

GenCore version 5.1.8
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OM protein - protein search, using sw model
 Run on: May 20, 2006, 22:15:21 ; Search time 195 Seconds
 (without alignments)

US-10-056-405-2
 Perfect score: 1973
 Sequence: 1 MVYNFKVKKCAPNGKVLY.....ADVETFRQDTIDQQASVDFE 383
 898.020 Million cell updates/sec

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2589679 seqs, 457216429 residues
 Total number of hits satisfying chosen parameters: 2589679
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_8:
 1: geneseq2005bs:
 2: geneseq1990s:
 3: geneseq2000s:
 4: geneseq2001s:
 5: geneseq2002s:
 6: geneseq2003as:
 7: geneseq2003bs:
 8: geneseq2004s:
 9: geneseq2005s:
 10: geneseq2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	5 ABP52833	Abp52833 Anopheles
2	1973	100.0	383	7 ABR84476	Abr84476 Mosquito
3	1384	70.1	364	4 ABB61736	Abb61736 Drosophili
4	1384	70.1	364	8 ADQ89588	Adq89588 Antagonis
5	1023	51.8	398	7 ABR84484	Abr84484 Mosquito
6	1002	50.8	470	4 ABB58174	Abb58174 Drosophil
7	982.5	49.8	401	4 ABB61964	Abb61964 Drosophili
8	907.5	46.0	410	4 AAG67780	Aag67780 Amino aci
9	903.5	45.8	418	4 AAG67778	Aag67778 Amino aci
10	903.5	45.8	452	5 ABC69495	Abg69495 Rat bait
11	900.5	45.6	418	5 ABG70174	Abg70174 Human pre
12	900.5	45.6	418	8 ADQ89786	Adq89786 Antagonis
13	897.5	45.5	418	4 AAG67779	Aag67779 Amino aci
14	890	45.1	369	4 ABG13574	Abg13574 Novel hum
15	885	44.9	382	4 AAG67785	Aag67785 An exempl
16	885	44.9	409	4 AAG67781	Aag67781 Amino aci
17	885	44.9	409	7 ADE58183	Ade58183 Human Pro
18	885	44.9	409	7 ADE58179	Ade58179 Human Pro
19	885	44.9	409	7 ADN95251	Adn95251 Human BBC
20	885	44.9	409	9 ADY15068	Ady15068 PRO polyp
21	885	44.9	479	10 AEF35190	Aef35190 Beta-gala
22	885	44.9	492	10 AEF35191	Aef35191 Beta-arre
23	880	44.6	409	4 AAG67784	Aag67784 An exempl

24	874	44.3	360	6 ADA00635	Ada00635 Human bet
25	874	44.3	495	6 ADA00637	Ada00637 Human bet
26	869.5	44.1	410	5 ABG69496	Abg69496 Rat bait
27	869.5	44.1	410	7 ADE58177	Ade58177 Rat Prote
28	869.5	44.1	410	7 ADE58181	Ade58181 Rat Prote
29	869.5	44.1	526	8 ADR23187	Adr23187 Yellow fl
30	869.5	44.1	526	8 ADR23188	Adr23188 Green flu
31	869.5	44.1	526	8 ADR23186	Adr23186 Yellow fl
32	865	43.8	454	8 ADN24049	Adn24049 Bacterial
33	796.5	40.4	382	9 ADY65950	Ady65950 S. manson
34	780.5	39.6	388	4 AAG67783	Aag67783 Amino aci
35	780.5	39.6	388	9 ADX07504	Adx07504 Cyclin-de
36	780	39.5	405	4 AAM78763	Aam78763 Human pro
37	779.5	39.5	388	4 AAG67782	Aag67782 Amino aci
38	767.5	38.9	394	9 AED51702	Aed51702 Pig arres
39	761	38.6	405	8 ADQ14327	Adq14327 Human ret
40	761	38.6	405	8 ADR41708	Adr41708 Protein s
41	761	38.6	405	9 AEB77788	Aeb77788 Human ret
42	723	36.6	405	9 AED51704	Aed51704 Pig S-ant
43	661	33.5	468	4 AAM79747	Aam79747 Human pro
44	516.5	26.2	182	7 ADD27419	Add27419 Human adi
45	516.5	26.2	182	7 ADD27127	Add27127 Human adi

ALIGNMENTS

RESULT 1
 ABP52833
 ID ABP52833 standard; protein; 383 AA.
 XX
 AC ABP52833;
 XX
 DT 01-NOV-2002 (first entry)
 XX
 DE Anopheles gambiae arrestin 1 protein SEQ ID NO:2.
 XX
 KW Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control; odourant receptor; olfaction.
 XX
 OS Anopheles gambiae.
 XX
 WO200259274-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 28-JAN-2002; 2002WO-US002549.
 XX
 PR 26-JAN-2001; 2001US-0264649P.
 PR 24-JAN-2002; 2002US-00056405.
 XX
 PA (UWVA-) UNIV VANDERBILT.
 XX
 PI Zwiebel LJ;
 XX
 DR WPI; 2002-627421/67.
 DR N-PSDB; ABQ5102.
 XX
 PT New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, or for identifying pest control agents.
 XX
 PT Claim 18; Fig 2; 96pp; English.
 XX
 CC The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence

(see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its complement; and (2) a method for identifying an agent that binds to mosquito olfaction molecules comprising: (a) providing an isolated mosquito olfaction molecule; (b) contacting a test agent with the isolated mosquito olfaction molecule; and (c) detecting specific binding of the test agent to the isolated mosquito olfaction molecule, where the presence of specific binding identifies the test agent as a mosquito olfaction-binding compound. The mosquito olfaction molecules are useful for mosquito management, i.e. controlling this pest and disease vector. A method from the present invention of screening for substances that modulate arrestin-odorant receptor interaction is useful for identifying pest control agents. The present sequence represents *Anopheles gambiae* arrestin 1 from the present invention

CC

XX

SQ

Sequence 383 AA;

Query Match 100.0%; Score 1973; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 3.9e-197;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVFKKCAPNGKVTLYMGKRDVFHDVSGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60
Db 1 MVYNFKVFKKCAPNGKVTLYMGKRDVFHDVSGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60
QY 61 FRYGREEDEVMGLNFOKECLCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
Db 61 FRYGREEDEVMGLNFOKECLCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
QY 121 PNAPSSVTLQOQGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 121 PNAPSSVTLQOQGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
QY 181 QPCTLVRKDFFMLSPGELELEVTLDKQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
Db 181 QPCTLVRKDFFMLSPGELELEVTLDKQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
QY 241 VVLFQNGSYRNTVASLETSGCPIQPGSSLOKVMYLTPLLSSNKQRGGIALDGQIKRQQ 300
Db 241 VVLFQNGSYRNTVASLETSGCPIQPGSSLOKVMYLTPLLSSNKQRGGIALDGQIKRQQ 300
QY 301 CLASTILLAQPDDQDRAFTGFGVIIYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVIIHA 360
Db 301 CLASTILLAQPDDQDRAFTGFGVIIYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVIIHA 360
QY 361 DSQADVETFRQDTIDQOASVDFE 383
Db 361 DSQADVETFRQDTIDQOASVDFE 383

RESULT 2

ABR84475

ID ABR84476 standard; protein; 383 AA.
XX AC ABR84476;
XX DT 15-JAN-2004 (first entry)
XX DE Mosquito olfaction molecule, arrestin 1.
XX KW Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
XX OS Anopheles gambiae.
XX PN WO2003076590-A2.
XX PD 18-SEP-2003.
XX PF 10-MAR-2003; 2003WO-US007174.
XX PR 08-MAR-2002; 2002US-00094240.
XX PA (UVVA-) UNIV VANDERBILT.

PI Zwiebel LJ;

XX

DR

N-PSDB;

ACF79716.

XX

PT

New mosquito

arrestin

1 and

2 genes

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QY 301 CLASTTLLAQPDQDAFGVIIISYAVKVKLFLGALGELSAELPFVLMHPKPGTKAKVHA 360
Db 300 ALASTTLIASQDARDAGFIVSYAVKVKLFLGALGELCAELPFILMPKPSRKAQL-- 356

QY 361 DSQADVE 367
Db 357 EAEGSIE 363

RESULT 5

ABR84484
ID ABR84484 standard; protein; 398 AA.
XX
AC ABR84484;
XX
DT 15-JAN-2004 (first entry)

Mosquito olfaction molecule, arrestin 2.

DE XX
KW Arrestin 2; mosquito; olfaction; insecticide; antimalarial.
XX Anopheles gambiae.

XX
FH Key Location/Qualifiers
FT Misc-difference 152 /note= "Encoded by AG"
FT WO2003076590-A2.
PN XX
PD 18-SEP-2003.
XX
PR 10-MAR-2003; 2003WO-US007174.
XX
PR 08-MAR-2002; 2002US-00094240.
XX
PA (UVVA-) UNIV VANDERBILT.
XX
PI Zwiebel LJ;
XX DR N-PSDB; ACF79731.
XX
PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
XX
PS Claim 16; Fig 12b; 101pp; English.

The present sequence is the protein sequence of arrestin 2, a novel mosquito olfaction molecule. The invention provides 9 novel mosquito polypeptides and the nucleic acids encoding them. These are arrestins 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function in a ligand-induced signal transduction pathway for the activation of mosquito olfaction. Arrestin functions to inhibit the activated signal transduction cascade. Thus, the odorant receptors act as an 'on' switch, and arrestin as an 'off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere with the operation of the mosquito olfactory system, particularly compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate sources of bloodmeal.

CC
XX Sequence 398 AA;

Query Match 51.8%; Score 1023; DB 7; Length 398;
Best Local Similarity 52.3%; Pred. No. 1.4e-97;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

QY 1 MVVNFKVKKCAPNGKVTLYMGKRDVFVHDHVGVEPIDGVVLDDEYIRDNRKVFGQIVCS 60
1 MVVAVKVKKSAPNGKLTVLGKRDFDHTDYCDPDPGVIVLDEEYL-RGRKVFGQLIT 59

Db 60 VRYGREEDEVMGVKFSKEMVLTKEQIYPM-ENANMEMTPMQRERLVKKLGANAAPPFTFHFP 118

QY 121 PNAQSSVTIQQGEDDNGDRCGVSYVVKI PAGESETDRTHRSTVTLGIRKIQAPTKQG 180
Db 119 SMAPSSVTLOAGEDDTGKPLGVEXAIAKAVGEDESOKGHKRSAVTLTIKKLQYAPVSRGR 178

QY 181 Q-PCTLVRKDFMLSPGELELEVTLDKOVLJGERIGVNICIRNNSNKMKVKKAMVQCV 239
Db 179 RLPSLVLVKSGKFTPSQGKINLLEVTLDRETVYHGKIAANIIVTNNSRKTVKSIKFVQHC 238

QY 240 DVVLFQNGSYRNTVASLETSECCTIOPGCSSLQKVMVLTPLSSNKQRGGIALDGOIKRQD 299
Db 239 EVTMV-NAQFSKHISLETREGCOPITPGASFTKSSFLVPLASSNKDRRGIAIDGHLKEDD 297

QY 300 QCLASTTLLAQPD-QRDAFGVIIISYAVKVKLFLGALGELSAELPFVLMHPKPGT--KAK 356
Db 298 VNLAASSTLISEGKCPSDAMGIVVISYSLRKVUNCGTIGELOTDVPKLMNPAPGSVERER 357

QY 357 VHADSQADVETFRQDT---IDQQASVDFE 383
Db 358 VNALKKMKSIERRHYENSHYADDNNIVFE 387

RESULT 6

ABB58174
ID ABB58174 standard; protein; 470 AA.
XX
AC ABB58174;
XX
DT 26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 1314.

DE XX
KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

KW OS Drosophila melanogaster.
XX PN WO20171042-A2.
XX PD 27-SEP-2001.
XX PR 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PR Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
DR N-PSDB; ABL02277.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

PT Disclosure; SEQ ID NO 1314; 21pp + Sequence Listing; English.

XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 470 AA;

Query Match 50.8%; Score 1002; DB 4; Length 470;
 Best Local Similarity 53.7%; Pred. No. 2.9e-95;
 Matches 187; Conservative 70; Mismatches 87; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLIMGKRDVFVHDHSGVEPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
 DB 48 RVEFKSSSNKGKITVYLGRDFDVHVTWVDPIDGVFVPEYVKD-RKVFGQVLAFFRYGR 106

QY 66 EEDEVWGLNFOKECLASEQIYPRPEKSDEQTKLQERLKKLGSNAIPFTFNISPNA 125
 DB 107 EDLDVLGLTFRKDLYLAHEQIYP-PWQDLPWTRLQERLIKLLGPNAHPFYFEVPPYCPA 165

QY 126 SVTLQQGEDDNGDCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTL 185
 DB 166 VSLSQPAPGDVGKSCGVDVYELKAFCVGENVEDKPKHRSVRLTIRKVMYAPSKVGEQPSIE 225

QY 186 VRKDFMLSPGELELETVLDKOLYLGERIGVNICIRNNSNKMKVKKIKAMVQGVQDVLFQ 245
 DB 226 VSKEFMMKPNKIHLEATLDKELYHGKISVNHVANNNSNRTVKKIKVCVRQPADICLFS 285

QY 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSNSNKORRGIALDQIKRQDOCLAST 305
 DB 286 TAQYKSVAEIESEDGCQVAPGFTISKVFCPLANNKDKWGLADGQQLKHEDTNLASS 345

QY 306 TLLAQPDQDAFGVILISYAVKVKFLFLGA--LGGEELSALPFLVMPK 351
 DB 346 TLITNPQAQRESLGIMVHYKVKVLLISSPLINGDLVAELPFTLMHPKP 393

RESULT 7

ID ABB61964 standard; protein; 401 AA.
 XX ABB61964;
 AC XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 12684.
 KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 KW Drosophila melanogaster.

PN WO200171042-A2.
 XX 27-SEP-2001.
 PD XX
 PR 23-MAR-2001; 2001WO-US009231.
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL06067.

XX Disclosure; SEQ ID NO 12684; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA

CC sequences (ABLI01840-ABLI6175) and the encoded proteins (ABBS5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 401 AA;

QY 1 MVYNFKVKKKCAPNGKVTLIMGKRDVFVHDHSGVEPIDGIVVLDEYIRDNRKVFGQIVCS 60
 DB 1 MVVSVVKFKKATPNGKVTFYLGRRDFIDHIDYCDPVDGVIVVEPDYLK-NRKVFGQVATT 59

QY 61 FRYGREEDEVMGLNFOKECLASEQIYPRPEKSDEQTKLQERLKKLGSNAIPFTFNIS 120
 DB 60 YRYGRIEDEVGMGVKFKSKELILCIREQIVPM-TNPMENTPMQEKLVRLKGSNAIPFTFHFP 118

QY 121 PNAPSSVTLOQGEDDNGDCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
 DB 119 PNSSPVSVTLOQEGDDNGKPKLGVETYTRAFVGDSBDDRQHKESMSVLVIKLOYAPLNRGQ 178

QY 181 Q-PCTLVRKDFMLSPGELELETVLDKOLYLGERIGVNICIRNNSNKMKVKKIKAMVQGV 239
 DB 179 RLPSLVLVKSGFTFSNGKISLEVTLDREIYHGKETAATVQVSNNSKKSIVCFIVQHT 238

QY 240 DVVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLISSNKORRGIALDQIKRQD 299
 DB 239 EITMV-NAQFSKHKVALETKEGCPITPGANLTKTFYLIPLAANNKDRHGGIALDGHILDED 297

QY 300 QCLASTLIAO-PDQDAFGVILISYAVKVKFLFLGAELPFLVMPKGT---- 353
 DB 298 VNLASSTMVQEGKSTGDAKGIVVISYSVRKLNCCTLUGEMQTDVPEFKLIQPAPGTIEKKR 357

QY 354 ---KAKVTHADSQADVENTFRQDTIDQQAQSVDF 382
 DB 358 SNAMKKMKSIEQHRNVKGYQDDDDNIVFSD 389

RESULT 8

AAG67780 standard; protein; 410 AA.
 ID AAG67780
 XX AC AAC67780;
 XX DE Amino acid sequence of human beta-arrestin 1B.
 XX DT 10-DEC-2001 (first entry)
 DE Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism; KW KW neurological disorder.
 XX Homo sapiens.
 OS XX
 EH Key Location/Qualifiers
 FT Region 155..184
 /note= "putative phosphorylation-recognition region"
 XX RN WO200167106-A2.
 XX PD 13-SEP-2001.
 XX FT 05-MAR-2001; 2001WO-US007304.
 PR 03-MAR-2000; 2000US-0186706P.
 XX PA (MILL-) MILLENNUM PHARM INC.
 XX

Qy 126 SVTLQQGEDDNGDPGCVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 126 SVTLQGPEDTGKACGVDEVKAFCAGENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185
 CC
 Qy 186 VRKDFMLSPGELELEVTLDKQOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQOGDVULFO 245
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 186 TTRQFLMSDKPLHLEASLDKRIYHGEPISVNVHVTNTNKTVKKIKISVROYADICLFN 245
 CC
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPPLISSNKORRGIALDGOIKRODOCLAST 305
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYLTPEFLANNREKGGLDGLKLIKEDTNLASS 303
 CC
 Qy 306 TLLAQPDORDAAGFVIIYAVKVKLFL--GALGGELSA----ELPFVLMHMPKPGTK--A 355
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 304 TLREGANREILGIVSYKVVKLVVSRGGLGDLASSDVAELPFTLMHPKKEEPPHR 363
 CC
 Qy 356 KVIAHDSDQADVENTFRODTID 375
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 364 EVPEHETPVDTNLIELDTND 383
 CC
 RESULT 10
 ABG69495
 ID ABG69495 standard; protein; 452 AA.
 XX
 AC ABG69495;
 XX
 DT 21-OCT-2002 (first entry)
 DE Rat bait protein beta arrestin 1.
 XX
 KW Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
 XX
 OS Rattus sp.
 XX
 PN WO200253726-A2.
 XX
 PD 11-JUL-2002.
 XX
 PR 02-JAN-2001; 2001US-0259377P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 DR N-PSDB; ABS51031.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interaction useful for treating obesity and metabolic disorders.
 XX
 PS Claim 1; Page 52; 125pp; English.
 XX
 CC The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the 'bait protein' in the yeast two- hybrid assay.

CC Sequence 452 AA;

Query Match 45.8%; Score 903.5; DB 5; Length 452;
 Best Local Similarity 47.1%; Pred. No. 5.7e-85;
 Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

Db 6 KVFKKCAPNGKVTLYMGKRDVFHDHVSGVEPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
 7 RVFKKASPNGLKLTVYLGKRDVFHDHVSGVEPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65

Qy 66 EEDEVWGLNFOKELCASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPNA 125
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 66 EDLDVLGLTFRKDLFVANWQSFPAPPDKPLTRIQLQERLLKKLGSNAIPFTFNISPNA 125

Qy 126 SVTLQQGEDDNGDPGCVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 126 SVTLQGPEDTGKACGVDEVKAFCAGENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185

Qy 186 VRKDFMLSPGELELEVTLDKQOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQOGDVULFO 245
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 186 TTRQFLMSDKPLHLEASLDKRIYHGEPISVNVHVTNTNKTVKKIKISVROYADICLFN 245

Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPPLISSNKORRGIALDGOIKRODOCLAST 305
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYLTPEFLANNREKGGLDGLKLIKEDTNLASS 303

Qy 306 TLLAQPDORDAAGFVIIYAVKVKLFL--GALGGELSA----ELPFVLMHMPKPGTK--A 355
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 304 TLREGANREILGIVSYKVVKLVVSRGGLGDLASSDVAELPFTLMHPKKEEPPHR 363

Qy 356 KVIAHDSDQADVENTFRODTID 375
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 364 EVPEHETPVDTNLIELDTND 383

RESULT 11
 ABG70174
 ID ABG70174 standard; protein; 418 AA.
 XX
 AC ABG70174;
 XX
 DT 21-OCT-2002 (first entry)
 DE Human prey protein for Shigella ipaH9.8 #4.
 XX
 KW Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; Selected interacting domain; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200257303-A2.
 XX
 PD 25-JUL-2002.
 XX
 PR 11-JAN-2002; 2002WO-EP000777.
 XX
 PR 12-JAN-2001; 2001US-0261130P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P;

CC in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 369 AA;

Query Match 45.1%; Score 890; DB 4; Length 369;
Best Local Similarity 48.6%; Pred. No. 1.1e-83; Mismatches 100; Indels 6; Gaps 4;

Matches 171; Conservative 75; Mismatches 100; Indels 6; Gaps 4;

Qy 6 KVFKKCAPNGKVTLYMGKRDVFHDHVSGVVEPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKLTIVLGKRDVFHDLDVDPVGVLVDPPEYLKE-RRVYVTLTCAFRYGR 65

Qy 66 EDEEVMLNFOKELCLASEQIYPRPEKSDKEOTKLUQERLLKKLGSNAIPFTFNISPNA 125
Db 66 EDLDVLGLTFRKDLFVANVQSFPPAPEDKPLTRLQERLIKKEHAYPFTFEIPPNLPC 125

Qy 126 SVTLOQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGOOPCTL 185
Db 126 SVTLOQGPEDTGKACGVDEAKAENLEEKIHKRNSVGLVIRKVOYAPERPGPOPTAE 185

Qy 186 VRKFMLSPGELEVLTDKOLYLRGERIGVNICIRNNNSNKMKIKAMVQGVDDVLFQ 245
Db 186 TTRFLMSDKPLHLBASLDKEIYVHGEPISVNVHVTNTNTKTEVKIKISVRQYADICLFN 245

Qy 246 NGSYRNTVASLETSEGCPQPGSSLQKVNLTPLLSNKORRGIALDGQIKRQDOCLAST 305
Db 246 TAQYKCPVAMEEADD--TVAPSSTFCVKYTITPFLANNREKRGALDGKLUKHEDTNLASS 303

Qy 306 TLLAQPDQDAFGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKP--GTKA 355
Db 304 TLREGANREILGIIVSYVKVKLVV-SRGGDVAVELPFTLMHPKAQRGTPA 354

RESULT 15

AAG67785
ID AAG67785 standard; protein; 382 AA.

XX AAG67785;
AC AAG67785;

DT 10-DEC-2001 (first entry)

DE An exemplary phosphorylation-independent arrestin mutant.

KW Arrestin; phosphorylation-independent arrestin mutant; retinitis pigmentosa; G protein-coupled receptor; GPCR; GPCR ligand; nephrogenic diuretic; stationary night blindness; colour blindness; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism; neurological disorder.

OS Unidentified.

XX WO200167106-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US007304.

XX PR 03-MAR-2000; 2000US-0186706P.
XX PA (MILL-) MILLENNUM PHARM INC.
XX PI Bernstein G;
XX DR WPI; 2001-602637/68.
XX PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX PS Disclosure; Page 47; 47pp; English.

The present sequence represents an exemplary phosphorylation-independent ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a test compound; and determining the ability of the test compound to modulate binding of arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs. The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists

XX Sequence 382 AA;

Query Match 44.9%; Score 885; DB 4; Length 382;
Best Local Similarity 48.3%; Pred. No. 3.8e-83; Mismatches 98; Indels 4; Gaps 3;

Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

Qy 6 KVFKKCAPNGKVTLYMGKRDVFHDHVSGVVEPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTIVLGKRDVFHDLDKVDPVGVLVLPDYLKD-RKVVFVTLCAFRYGR 66

Qy 66 EDEEVMLNFOKELCLASEQIYPRPEKSDKEOTKLUQERLLKKLGSNAIPFTENISPNA 125
Db 67 EDLDVLGLSFRKDLFIATYQAFFPVNPVPPRPTRLQDRLLRKLGQAHPPFFTIPQNLP 126

Qy 126 SVTLOQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGOOPCTL 185
Db 127 SVTLOQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNNSVRLVIRKVOAPEKPGPQPSAE 186

Qy 186 VRKFMLSPGELEVLTDKOLYLRGERIGVNICIRNNNSNKMKIKAMVQGVDDVLFQ 245
Db 187 TTRFLMSDRSLHLEASLDKELYVHGEPLNTVHVNNTKTKVKKIVSVRQYADICLFN 246

Qy 246 NGSYRNTVASLETSEGCPQPGSSLQKVNLTPLLSNKORRGIALDGQIKRQDOCLAST 305
Db 247 TAQYKCPVAMEEADD--QVSPSSTFCVKYTITPFLANNREKRGALDGKLUKHEDTNLASS 304

Qy 306 TLLAQPDQDAFGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
Db 305 TIVKEGANKEVLGLVILSYVRVKVLVV-SRGGDVSVELPFTLMHPKP 349

Search completed: May 20, 2006, 22:26:20
Job time : 198 secs

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2006, 22:44:57 ; search time 41 Seconds
 Perfect score: 1973
 Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVENTFRODTIDQQASVDDE 383
 (without alignments)
 898.805 Million cell updates/sec

Title: US-10-056-405-2
 Scoring table: Gapop 10.0 , Gapext 0.5
 Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1499	76.0	381	2 B56607	arrestin homolog -
2	1384	70.1	364	2 A34867	arrestin - fruit f
3	1335	67.7	363	2 A55081	arrestin 1 - blueb
4	993.5	50.4	407	2 A56607	arrestin homolog -
5	977.5	49.5	401	2 S11566	49K photoreceptor
6	975.5	49.4	401	2 A34856	arrestin 2 - blueb
7	942.5	47.8	401	2 B55081	beta-arrestin, bra
8	903.5	45.8	418	2 A34851	beta-arrestin1 - r
9	903.5	45.8	418	2 B43404	beta-arrestin1, s
10	891.5	45.2	418	2 B46682	arrestin arr3L - b
11	887	45.0	420	2 A47140	arrestin - human (
12	882	44.7	409	2 S18984	arrestin isoform 1
13	871	44.1	407	2 S68253	beta-arrestin 2 -
14	869.5	44.1	410	2 A59279	hypothetical prote
15	865	43.8	454	2 T34297	arrestin isoform 1
16	863	43.7	415	2 S68255	arrestin isoform 2
17	861	43.6	405	2 S68254	cone arrestin - Af
18	810	41.1	387	2 I51404	cone arrestin - bu
19	785.5	39.8	389	2 S68175	cone arrestin - no
20	784.5	39.8	389	2 S68172	S-antigen - mouse
21	783.5	39.7	403	2 JS0066	arrestin - human
22	780.5	39.6	388	2 S38943	S-antigen - rat
23	775.5	39.3	403	2 S03960	S-antigen - bovine
24	768.5	39.0	404	2 A28404	retinal S-antigen
25	761	38.6	405	2 A30357	rod arrestin - nor
26	731.5	37.1	396	2 S68173	arrestin-C - human
27	731	37.1	387	2 I55423	rod arrestin - bul
28	729.5	37.0	396	2 S68174	C-arrestin - rat (
29	134	6.8	92	2 I70113	

30 129 6.5 378 2 T28112 hypothetical prote
 31 118.5 6.0 427 2 T23954 hypothetical prote
 32 111.5 5.7 364 2 T26507 hypothetical prote
 33 111.5 5.7 471 2 T15155 splicing factor PR
 34 111.5 5.7 2413 2 S34670 hypothetical prote
 35 110.5 5.6 344 2 T33421 hypothetical prote
 36 110 5.6 456 2 T29948 hypothetical prote
 37 107.5 5.4 312 2 T20949 hypothetical prote
 38 107.5 5.4 460 2 T23955 hypothetical prote
 39 106.5 5.4 460 2 T33420 hypothetical prote
 40 106 5.4 347 2 S31144 nestin - golden ha
 41 104 5.3 338 2 F87145 probable ribonucle
 42 102.5 5.2 454 2 T16826 Ku antigen 70K cha
 43 101.5 5.1 1804 2 T34518
 44 100 5.1 359 2 B70534
 45 99.5 5.0 600 2 S65788

ALIGNMENTS

RESULT 1
 B56607
 arrestin homolog - tobacco budworm
 C;Species: Heliothis virescens (tobacco budworm)

C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C;Accession: B56607 R;Raming, K.; Freitag, J.; Krieger, J.; Breer, H.

Cell. Signal. 5, 69-80, 1993

A;Title: Arrestin-subtypes in insect antennae.

A;Reference number: A56607; MUID:93199955; PMID:8452755

A;Accession: B56607 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A;Molecule type: mRNA A;Residues: 1-381 <RAM>

A;Cross-references: UNIPROT:P55274; UNIPARC:UPI0000126089 A;Experimental source: antennae

A;Note: sequence extracted from NCBI backbone (NCBIP:127926) C;Superfamily: arrestin

Query Match 76.0%; Score 1499; DB 2; Length 381;

Best local Similarity 72.7%; Pred. No. 1.2e-110; Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;

Qy 1 MVYNFKVFKKCAPNGKVTLYMGKRDFFDHVSGVEPIDGIVVLDDDEVYIRDNRKVFGQIVCS 60
 Db 1 MVYNFKVFKKCAPNGKVTLYMAKRDFFDHISTVEPIDGIVVLDEEYVR-GRKVFGQMCR 59

Qy 61 FRYGREEDEVMLGLNQFQELCLASEQIYPRPEKSDEQTKLQERLLKKLGSSNAIPFTENS 120
 Db 60 FRYGREEDEVMLGLNQFYKEPLASBQIYPPPEKRKNELSRTQERLIKGDGAIPFRLTVP 119

Qy 121 PNAPSSVTLQOGEDDNGDPGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTQKGQ 180
 Db 120 PGAGPSVILQGLEDDGEPCGVQYVVKTFVGDSIDRSRRSTVALGIRKQYAPAKGP 179

Qy 181 QPCTLVKDFMLSPGELELETVLTDKQLYLGERIGVNICIRNNSNKMKVKKIKAMVQGVD 240
 Db 180 QPCTVVKDFVLSPGQLEELTLDKQLYHGETVAVMCVRNHSNKVKVKKIKACIQGVD 239

Qy 241 VVLFQNGSYRNTVASLETSGCGPIOPGSSLQKVNQRRGIALDGQIKRQDQ 300
 Db 240 VVLFQNGQYRNIVASIEQTQDGCPQLQPSLQKVLHLPTLAHNRDKRGIAIDGQIKRSRT 299

Qy 301 CLASTLILAOPDQDRAFTGVIISAVKVLFLGALGGELSAELPFVLMHPKPGTKAKVHA 360
 Db 300 TLASTLILDPDORDAFGIVWVSYSAKVKVXVLGAISGELVAELPFILMHPKEG-RVVKVHA 358

Qy 361 DSOQADVENTFRODTIDQQASVD 381
 Db 359 DSQADVEMFRODTVHHQESVE 379

RESULT 5

S11566 arrestin homolog - fruit fly (*Drosophila miranda*)
 C;Species: *Drosophila miranda*
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S11566
 R;Krishnan, R.; Ganguly, R.
 Nucleic Acids Res. 18, 5894, 1990
 A;Title: Nucleotide sequence of the arrestin-like 49 kDa protein gene of *Drosophila miranda*
 A;Reference number: S11566; MUID:91016944; PMID:2216789
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-401 <KRI>
 A;Cross-references: UNIPROT:P19108; UNIPARC:UPI0000126081; EMBL:X54084; NID:97612; PIDN:
 C;Genetics:
 A;Gene: FlyBase:Arr2
 A;Cross-references: FlyBase:FBgn0000121
 C;Superfamily: arrestin

Query Match 49.4%; Score 975.5; DB 2; Length 401;
 Best Local Similarity 48.5%; Pred. No. 2.7e-69; Mismatches 115; Indels 13; Gaps 6;
 Matches 190; Conservative 74; Mismatches 115; Indels 13; Gaps 6;

Qy 1 MVYNFKVKKCARNGKVLYMNGKRDVFHDVSGVEPIDGIWVLDEYIRDNRKVRGQIVCS 60
 Db 1 MVVSVKVKFKATPNCVKTFYLGRDFDIDHIDYCDPVDGIVVNPEDYLN-NRKVFGQIATT 59

Qy 61 FRYGREDEEVMLNFFQKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNIS 120
 Db 60 YRYGREDEEVMGVKFKSKELLICREQIVPM-TNPNMEMTPMOEKLVRKGSSAHPPFTFHFP 118

Qy 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESEETDRTHRSTVTLGIRKIQFAPTKOGO 180
 Db 119 PNSPSSVTLQQEGDDNGKPLGVEYTIRAFVGDSEDDROKRSMVSLVIKKLQYAPLNRGQ 178

Qy 181 Q-PCTLVRKDFMLSPGELELEVTLDKOLYLGGERIGVNICIRNNNSNKVKIKAMVQGV 239
 Db 179 RLPSSLVSKGKFTFSNGKISLEVTLDREIYHGKEKTAATQVSNNSKSKVSKSICKFTIVOHT 238

Qy 240 DVVLFQNGSYRNTVASLETSEGCPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRD 299
 Db 239 EITMV-NAQFSKHKVAOLETKEGCCPITPGANLTKTFLYLIPLAANNKDRGIALDGHLKDED 297

Qy 300 OCLASTTLLAQ-PDORDA邢FGVITISYAVKVFLGALGGELSABELPPVLMMPKGT---- 353
 Db 298 VNLAASSTMVQEGKSKTGACGIVIVSYSVRIKLNCGTLGGEQMDTVPFKLQAPGTEKRR 357

Qy 354 ---KAKVITHADSOADVETFRQDTIDQQASVDF 382
 Db 358 SNAMEKOMKSIEQHRNVKGYYQDDDDNTIVFEDF 389

RESULT 6

A34856 49K photoreceptor protein - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 C;Accession: A34856
 R;Yamada, T.; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto, I.
 Science 248, 483-485, 1990
 A;Title: A 49-kilodalton phosphoprotein in the *Drosophila* photoreceptor is an arrestin homolog
 A;Reference number: A34856; MUID:90232360; PMID:2158671
 A;Accession: A34856
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-401 <YAM>
 A;Cross-references: UNIPROT:P19107; UNIPARC:UPI0000126081; EMBL:X54084; NID:9158157; PIDN:
 C;Genetics:
 A;Gene: FlyBase:Arr2
 A;Cross-references: FlyBase:FBgn0000121
 C;Superfamily: arrestin

Query Match 49.4%; Score 975.5; DB 2; Length 401;
 Best Local Similarity 48.5%; Pred. No. 2.7e-69; Mismatches 115; Indels 13; Gaps 6;
 Matches 190; Conservative 74; Mismatches 115; Indels 13; Gaps 6;

Qy 1 MVYNFKVKKCARNGKVLYMNGKRDVFHDVSGVEPIDGIWVLDEYIRDNRKVRGQIVCS 60
 Db 1 MVVSVKVKFKATPNCVKTFYLGRDFDIDHIDYCDPVDGIVVNPEDYLN-NRKVFGQIATT 59

Qy 61 FRYGREDEEVMLNFFQKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNIS 120
 Db 60 YRYGREDEEVMGVKFKSKELLICREQIVPM-TNPNMEMTPMOEKLVRKGSSAHPPFTFHFP 118

Qy 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESEETDRTHRSTVTLGIRKIQFAPTKOGO 180
 Db 119 PNSPSSVTLQQEGDDNGKPLGVEYTIRAFVGDSEDDROKRSMVSLVIKKLQYAPLNRGQ 178

Qy 181 Q-PCTLVRKDFMLSPGELELEVTLDKOLYLGGERIGVNICIRNNNSNKVKIKAMVQGV 239
 Db 179 RLPSSLVSKGKFTFSNGKISLEVTLDREIYHGKEKTAATQVSNNSKSKVSKSICKFTIVOHT 238

Qy 240 DVVLFQNGSYRNTVASLETSEGCPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRD 299
 Db 239 EITMV-NAQFSKHKVAOLETKEGCCPITPGANLTKTFLYLIPLAANNKDRGIALDGHLKDED 297

Qy 300 OCLASTTLLAQ-PDORDA邢FGVITISYAVKVFLGALGGELSABELPPVLMMPKGT---- 353
 Db 298 VNLAASSTMVQEGKSKTGACGIVIVSYSVRIKLNCGTLGGEQMDTVPFKLQAPGTEKRR 357

Qy 354 ---KAKVITHADSOADVETFRQDTIDQQASVDF 382
 Db 358 SNAMEKOMKSIEQHRNVKGYYQDDDDNTIVFEDF 389

RESULT 7

B55081 arrestin 2 - bluebottle fly (*Calliphora vicina*)
 C;Species: *Calliphora vicina*
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C;Accession: B55081; S44292
 R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
 J. Biol. Chem. 269, 26969-26975, 1994
 A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
 A;Reference number: A55081; MUID:95014564; PMID:7929436
 A;Accession: B55081
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-401 <PLA>
 A;Cross-references: UNIPROT:P51487; UNIPARC:UPI000016B8DC; EMBL:X79073; NID:9483583; PID:
 C;Superfamily: arrestin

Qy 185 LVRKDFMLSPGELELEVTLDKOLYLGGERIGVNICIRNNNSNKVKIKAMVQGV 244
 Db 192 LVSKGFTESQGKINLEVTLDRREIYHGKEKTAATQVSNNSKSKVSKSICKFTIVOHT 238

Qy 245 ONGSYRNTVASLETSEGCPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRD 299
 Db 252 -NAQFSRHHVASLETREGCPITPGASFTKVFVLYPCAASNKDRGIALDGHLKDED 297

Qy 305 RTLLAQ-PDORDA邢FGVITISYAVKVFLGALGGELSABELPPVLMMPKGT---- 359
 Db 311 STLVSEGKNTDAIGIVISYSLRVKLNCGTIGELQTDVPEKLLHPAPGTAEREKAQAI- 369

Qy 360 ADSQADVETFRQD---TIDQQASVDF 383
 Db 370 -KKMKSIERTRYENSCYAADDNNIVFE 396

Best Local Similarity 47.7%; Pred. No. 1.1e-66; Matches 187; Conservative 70; Mismatches 122; Indels 13; Gaps 6; Db 66 EDLDVGLTFRKDLFVANVQSFPPAEDKKPLTRLQERLIKLUCEHAYPFTFEIPPNLPC 125

Qy 1 MVVNVKVFKKCAPNGKVTLYMGKRDFFDVRVSGVERIDGIVVLDEYIRDNRKVFGQIVCS 60
Db 1 MVVNVKVFKKATPNKGKTFYLGRRHFDYDIPDVGVIVVDPDYLK-NRKVFAQLATI 59

Qy 61 FRYGREGEEDEVMGLNFQKEKLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNIS 120
Db 60 YRGREEDEVMGVKFSKELILCREQIVPM-GNSNMEMPTQEKLVRLKGSNAHPFTFHFP 118

Qy 121 PNAPSSVTQLOGGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 119 PNSPSSVTQLOGGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Qy 181 Q-PCTLVRKDFMLSPGELELEVTLDKOLYLRGERIGVNICIRNNSNKMKKKAMVQGVDFLQ 245
Db 179 RLPSLSLVSKGFTPSNGKISLAVILDREIVVHGKVAATVQINNNSKAVKNIKVFIQHT 238

Qy 240 DVVLFQNGSYRNTVASLETSEGCPPIOPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQD 299
Db 239 EITMV-NAQPSKHKVALETKEGCIPFGANLSKTFYLIPLASNKDRHGIADGHLKD 297

Qy 300 QCLASTTLLAQ-PDQDAFGVIIISYAVKVKLFLGAGGELSAELPFVLMHPKPGT---- 353
Db 298 VNLAASSTMVQDGKSTGDAKGIVISYSVRIKLNCGTILGEIQTDVPKLQLQAPGSVEKKR 357

Qy 354 --KAKVIHADSQADVENTFRQDTIDQASVDF 382
Db 358 SNAMKKMSIEQHRTKGYYQDDDNIVFEDF 389

RESULT 8

A34851 beta-arrestin, brain - bovine

C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jul-1990 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C;Accession: A34851; JC2052
R;Lohse, M.J.; Benovic, J.L.; Codina, J.; Caron, M.G.; Lefkowitz, R.J.
Science, 248, 1547-1550, 1990.

A;Title: Beta-arrestin: a protein that regulates beta-adrenergic receptor function.
A;Reference number: A34851; MUID:90296080; PMID:2163110
A;Accession: A34851
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-418 <LOH>
A;Cross-references: UNIPROT:P17870; UNIPARC:UPI000042307; GB:M33601; NID:9162691; PIDN:
A;Experimental source: brain
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.R.
J. Biol. Chem., 268, 15640-15648, 1993
A;Title: Polypeptide variants of beta-arrestin and arrestin3.
A;Reference number: A47140; MUID:93340166; PMID:8340388
A;Accession: JC2052
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-15, 'C',17-30, 'L',32, 'K',34-83, 'Y',85-176, 'K',178-206, 'L',208-333, 342-418 <

Qy 6 KVFKKCAGNGKVTLYMGKRDFFDHSVSGVERIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKTFYLGKRDFFDHDIDLVPDVGVWVLPDEYK-RRVYVLTCAFRYGR 65

Qy 66 EEDEVMLNFQKEKLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTENISPNAPS 125
Db 66 EDLDVGLTFRKDLFVANVQSFPPAEDKKPLTRLQERLIKLUCEHAYPFTFEIPPNLPC 125

Qy 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
Db 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185

Qy 186 VRKDFMLSPGELELEVTLDKOLYLRGERIGVNICIRNNSNKMKKKAMVQGVDFLQ 245
Db 186 TTRQFLMSDKPLHLEASLDKELIYHGERISVNVHVVNTNKTKVKKIKISVQYADLFN 245

Qy 246 NGSYRNTVASLETSEGCPPIOPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQD 305
Db 246 TAQYKCPVAMEADD-TVAPSSTFCVKVYTLPFLANNREKRGGLADGKLKHEDTNLASS 303

Qy 306 TLLAQPDORDAFGVIIISYAVKVKLFL-GAGGELSAELPFVLMHPKPGT---A 355
Db 304 TLLREGANREILGIIVSYVKVKLVLVSRGGLGDIASSDVAVELPFTLMHPKPKKEEPHR 363

Qy 356 KVTHADSQADVENTFRQDTID 375
Db 364 EVPEHETPVDTNLIEDTN 383

RESULT 9

B43404 beta-arrestin1 - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B43404
R;Attramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder, J. Biol. Chem., 267, 17882-17890, 1992
A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A;Reference number: A43404; MUID:92388146; PMID:1517224
A;Accession: B43404
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-418 <ATT>
A;Cross-references: UNIPROT:P29066; UNIPARC:UPI0000126079; GB:M91589; NID:949985; PIDN:
A;Note: Sequence extracted from NCBI backbone (NCBIP:112791)
C;Superfamily: arrestin

Query Match Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418; Matches 178; Conservative 78; Mismatches 111; Indels 13; Gaps 5; Db 66 EDLDVGLTFRKDLFVANVQSFPPAEDKKPLTRLQERLIKLUCEHAYPFTFEIPPNLPC 125

Qy 6 KVFKKCAGNGKVTLYMGKRDFFDHSVSGVERIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKTFYLGKRDFFDHDIDLVPDVGVWVLPDEYK-RRVYVLTCAFRYGR 65

Qy 66 EEDEVMLNFQKEKLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTENISPNAPS 125
Db 66 EDLDVGLTFRKDLFVANVQSFPPAEDKKPLTRLQERLIKLUCEHAYPFTFEIPPNLPC 125

Qy 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
Db 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185

Qy 186 VRKDFMLSPGELELEVTLDKOLYLRGERIGVNICIRNNSNKMKKKAMVQGVDFLQ 245
Db 186 TTRQFLMSDKPLHLEASLDKELIYHGERISVNVHVVNTNKTKVKKIKISVQYADLFN 245

Qy 246 NGSYRNTVASLETSEGCPPIOPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQD 305
Db 246 TAQYKCPVAMEADD-TVAPSSTFCVKVYTLPFLANNREKRGGLADGKLKHEDTNLASS 303

Qy 306 TLLAQPDORDAFGVIIISYAVKVKLFL-GAGGELSAELPFVLMHPKPGT---A 355
Db 304 TLLREGANREILGIIVSYVKVKLVLVSRGGLGDIASSDVAVELPFTLMHPKPKKEEPHR 363

Qy 356 KVTHADSQADVENTFRQDTID 375
Db 364 EVPEHETPVDTNLIEDTN 383

RESULT 10

B46682 beta-arrestin 1, splice form A - human
N;Contains: beta-arrestin 1, splice form B
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 22-Sep-1993 #text_change 09-Jul-2004
C;Accession: B46682; A46682
R;Parruti, G.; Peracchia, F.; Sallese, M.; Ambrosini, G.; Masini, M.; Rotilio, D.; De Bl
J. Biol. Chem. 268, 9753-9761, 1993
A;Title: Molecular analysis of human beta-arrestin-1: cloning, tissue distribution, and
A;Reference number: A46682; MUID:93252853; PMID:8486659
A;Accession: B46682
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-418 <PAR1>
A;Cross-references: UNIPROT:P49407; UNIPARC:UPI000016A589; GB:L04685; NID:g347956; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIP:134014)
A;Accession: A46682
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Gene: GDB:ARRB1; ARR1
A;Cross-references: UNIPARC:UPI000016A58A; GB:L04685; NID:g347956; PIDN:AAA35558.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIP:134015)
C;Genetics:
C;Superfamily: arrestin
C;Keywords: alternative splicing

Query Match Best Local Similarity 45.2%; Score 891.5; DB 2; Length 418;
Matches 176; Conservative 78; Mismatches 113; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGRDFDHWVGSGVERPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKSPNCKLTIVLGKRDFFVDHLDKVDPDVGLVLPDPYKD-RKVFTVLTCAFRYGR 66

QY 66 EEDEVVMLNFOKECLCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTENISPNA 125
Db 67 EDLDPVGLSFRKDLF1ANYQAFPPPTNNPPRPPRTRLQERLLRKLGQHAAHPFFFTIPONUPC 126

QY 126 SVTLQQGEDDDNGDPCCGVSYVKIFAGESETDRRSTVTLGIRKIQFAPTKQGQQCPCTL 185
Db 127 SVTLQPGPEDTGKACGVDFEIRAFCAKSLEKSHRNNSVRLVIRKVQFAPKPGPQPSAE 186

QY 186 VRKDFMLSPGELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVDFVLFQ 245
Db 186 TTRHFLMSDRSLHLEASLDKBLYYHGERPLNVNHVTNNSTKTVKKIKVSQRYADICLFS 246

QY 246 NGSYRNTVASLETSEGCPPIQPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQDOCLAST 305
Db 247 TAQYKCPVAQEODD-QWSPSSTFCVTTTPLSNNNREKRGGLADGKLIKHDTNLASS 304

QY 306 TLLAQPDQDAFGVVISAVVKVLFQLAGGGELSAELPFVLMMPKPK 351
Db 305 TIVKEGANKEVLGILVSVYRVKVLVV-SRGGDVSVELPFVLMMPKPK 349

Db 126 SVTLQPGPEDTGKACGVDFEIRAFCAKSLEKSHRNNSVRLVIRKVQFAPKPGPQPSAE 185

QY 186 VRKDFMLSPGELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVDFVLFQ 245
Db 186 TTRHFLMSDRSLHLEASLDKBLYYHGERPLNVNHVTNNSTKTVKKIKVSQRYADICLFS 246

QY 246 NGSYRNTVASLETSEGCPPIQPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQDOCLAST 305
Db 247 TAQYKCPVAQEODD-QWSPSSTFCVTTTPLSNNNREKRGGLADGKLIKHDTNLASS 304

QY 306 TLLAQPDQDAFGVVISAVVKVLFQLAGGGELSAELPFVLMMPKPK 351
Db 305 TIVKEGANKEVLGILVSVYRVKVLVV-SRGGDVSVELPFVLMMPKPK 349

RESULT 11

A47140 arrestin arr3L - bovine
N;Contains: arrestin arr3S
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47140; B47140; JCB2051
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A
J. Biol. Chem. 268, 15640-15648, 1993

Query Match Best Local Similarity 44.7%; Score 882; DB 2; Length 409;
Matches 167; Conservative 76; Mismatches 99; Indels 4; Gaps 3;

QY 6 KVFKKKCAPNGKVTLYMGRDFDHWVGSGVERPIDGIVVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 8 RVFKKSPNCKLTIVLGKRDFFVDHLDKVDPDVGLVLPDPYKD-RKVFTVLTCAFRYGR 66

QY 66 EEDEVVMLNFOKECLCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTENISPNA 125

A;Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA
A: Residues: 1- Δ 64 \times

A;Cross-references: U

C;Genetics:

A;Gene: CESP;F53H8.2
A:Intron: 11/3:61/1

R, millions: 11, 2, 31, 1, 2; Superfamily: arrestin

Query Match Score 865; DB 2; Length 454;

	Index	Gap
Best Local Similarity	46.6%	pred. No. 1.7e-60;
Matches	174.	Mismatches 101;
Concordance	70.	

According to the author, the first step in the process of creating a new language is to identify the needs of the users. This involves understanding the specific requirements of the intended users, such as the size of the vocabulary, the complexity of the grammar, and the ease of learning and using the language.

QY
6 KVFKKCAPNGKVLYMGKRDVFV-----HVSGVEPID-----GIVWLDEY 46

DB
11 RVEKKTSPNGKTTIYLGKRDFIDRGDYVLDLIGENKGTEPONVGFILETGILSHGMWLVIDEY 70

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OY
47 IRDNRKVFGQIVCSFRYGRBEDEVMLNPKELCLASDQIYPREKS-DKEQIKLQERLL 105

Db
71 IKDNRKVTAAHLAAFRYGRBEDDVGLTFRKDLISETFQVYPTDKISRPLSSRLQERLK 130

THE AMERICAN POLITICAL SCIENCE ASSOCIATION 159

KLUGENNAFFEL IN DER KUNSTSCHAU IN DER GEGESENDELLER STRASSE 150

DB 131 RKLGANAAPPFWEEVAPKSASSVTLQAPGDTGKPCGVYELKTFAVTDGSSGG-KPKKS 189

159 HISTORIÆ CIPRI TERRÆ COOPTÆ VRCRDEMIS SPECIELE FESTIVITATIBUS 218

Db ALSNTVRLAIRKLYAPFESRPQPMVDMVKYMMSSGILHMEVSLDKEMYYHGESISVN 249

OY
219 CIRNNSNKMYKKIKAMVOOGVDPWLFONGSYRINTVASLETSEGCPIOPGSLOKMYMLTP 278

卷之三

DB 250 HIONNSNKTVKKLKIYIIOVADICLFETTASYSCEVARIESNEGFPPVPGGILSKVFAVCE 309

OY
279 LLSSNKQRGIALDQOKRQDQCLASTTLAQPDQRDAAFGVIIISYAVKVKLLFLGALGGEL 338

THE JOURNAL OF CLIMATE

UD 303 310 316 322 328 334 340 346 352 358 364 370 376 382 388 394 398 404 410 416 422 428 434 440 446 452 458 464 470 476 482 488 494 498 504 510 516 522 528 534 540 546 552 558 564 570 576 582 588 594 598 604 610 616 622 628 634 640 646 652 658 664 670 676 682 688 694 698 704 710 716 722 728 734 740 746 752 758 764 770 776 782 788 794 798 804 810 816 822 828 834 840 846 852 858 864 870 876 882 888 894 898 904 910 916 922 928 934 940 946 952 958 964 970 976 982 988 994 998 1004 1010 1016 1022 1028 1034 1040 1046 1052 1058 1064 1070 1076 1082 1088 1094 1098 1104 1110 1116 1122 1128 1134 1140 1146 1152 1158 1164 1170 1176 1182 1188 1194 1198 1204 1210 1216 1222 1228 1234 1240 1246 1252 1258 1264 1270 1276 1282 1288 1294 1298 1304 1310 1316 1322 1328 1334 1340 1346 1352 1358 1364 1370 1376 1382 1388 1394 1398 1404 1410 1416 1422 1428 1434 1440 1446 1452 1458 1464 1470 1476 1482 1488 1494 1498 1504 1510 1516 1522 1528 1534 1540 1546 1552 1558 1564 1570 1576 1582 1588 1594 1598 1604 1610 1616 1622 1628 1634 1640 1646 1652 1658 1664 1670 1676 1682 1688 1694 1698 1704 1710 1716 1722 1728 1734 1740 1746 1752 1758 1764 1770 1776 1782 1788 1794 1798 1804 1810 1816 1822 1828 1834 1840 1846 1852 1858 1864 1870 1876 1882 1888 1894 1898 1904 1910 1916 1922 1928 1934 1940 1946 1952 1958 1964 1970 1976 1982 1988 1994 1998 2004 2010 2016 2022 2028 2034 2040 2046 2052 2058 2064 2070 2076 2082 2088 2094 2098 2104 2110 2116 2122 2128 2134 2140 2146 2152 2158 2164 2170 2176 2182 2188 2194 2198 2204 2210 2216 2222 2228 2234 2240 2246 2252 2258 2264 2270 2276 2282 2288 2294 2298 2304 2310 2316 2322 2328 2334 2340 2346 2352 2358 2364 2370 2376 2382 2388 2394 2398 2404 2410 2416 2422 2428 2434 2440 2446 2452 2458 2464 2470 2476 2482 2488 2494 2498 2504 2510 2516 2522 2528 2534 2540 2546 2552 2558 2564 2570 2576 2582 2588 2594 2598 2604 2610 2616 2622 2628 2634 2640 2646 2652 2658 2664 2670 2676 2682 2688 2694 2698 2704 2710 2716 2722 2728 2734 2740 2746 2752 2758 2764 2770 2776 2782 2788 2794 2798 2804 2810 2816 2822 2828 2834 2840 2846 2852 2858 2864 2870 2876 2882 2888 2894 2898 2904 2910 2916 2922 2928 2934 2940 2946 2952 2958 2964 2970 2976 2982 2988 2994 2998 3004 3010 3016 3022 3028 3034 3040 3046 3052 3058 3064 3070 3076 3082 3088 3094 3098 3104 3110 3116 3122 3128 3134 3140 3146 3152 3158 3164 3170 3176 3182 3188 3194 3198 3204 3210 3216 3222 3228 3234 3240 3246 3252 3258 3264 3270 3276 3282 3288 3294 3298 3304 3310 3316 3322 3328 3334 3340 3346 3352 3358 3364 3370 3376 3382 3388 3394 3398 3404 3410 3416 3422 3428 3434 3440 3446 3452 3458 3464 3470 3476 3482 3488 3494 3498 3504 3510 3516 3522 3528 3534 3540 3546 3552 3558 3564 3570 3576 3582 3588 3594 3598 3604 3610 3616 3622 3628 3634 3640 3646 3652 3658 3664 3670 3676 3682 3688 3694 3698 3704 3710 3716 3722 3728 3734 3740 3746 3752 3758 3764 3770 3776 3782 3788 3794 3798 3804 3810 3816 3822 3828 3834 3840 3846 3852 3858 3864 3870 3876 3882 3888 3894 3898 3904 3910 3916 3922 3928 3934 3940 3946 3952 3958 3964 3970 3976 3982 3988 3994 3998 4004 4010 4016 4022 4028 4034 4040 4046 4052 4058 4064 4070 4076 4082 4088 4094 4098 4104 4110 4116 4122 4128 4134 4140 4146 4152 4158 4164 4170 4176 4182 4188 4194 4198 4204 4210 4216 4222 4228 4234 4240 4246 4252 4258 4264 4270 4276 4282 4288 4294 4298 4304 4310 4316 4322 4328 4334 4340 4346 4352 4358 4364 4370 4376 4382 4388 4394 4398 4404 4410 4416 4422 4428 4434 4440 4446 4452 4458 4464 4470 4476 4482 4488 4494 4498 4504 4510 4516 4522 4528 4534 4540 4546 4552 4558 4564 4570 4576 4582 4588 4594 4598 4604 4610 4616 4622 4628 4634 4640 4646 4652 4658 4664 4670 4676 4682 4688 4694 4698 4704 4710 4716 4722 4728 4734 4740 4746 4752 4758 4764 4770 4776 4782 4788 4794 4798 4804 4810 4816 4822 4828 4834 4840 4846 4852 4858 4864 4870 4876 4882 4888 4894 4898 4904 4910 4916 4922 4928 4934 4940 4946 4952 4958 4964 4970 4976 4982 4988 4994 4998 5004 5010 5016 5022 5028 5034 5040 5046 5052 5058 5064 5070 5076 5082 5088 5094 5098 5104 5110 5116 5122 5128 5134 5140 5146 5152 5158 5164 5170 5176 5182 5188 5194 5198 5204 5210 5216 5222 5228 5234 5240 5246 5252 5258 5264 5270 5276 5282 5288 5294 5298 5304 5310 5316 5322 5328 5334 5340 5346 5352 5358 5364 5370 5376 5382 5388 5394 5398 5404 5410 5416 5422 5428 5434 5440 5446 5452 5458 5464 5470 5476 5482 5488 5494 5498 5504 5510 5516 5522 5528 5534 5540 5546 5552 5558 5564 5570 5576 5582 5588 5594 5598 5604 5610 5616 5622 5628 5634 5640 5646 5652 5658 5664 5670 5676 5682 5688 5694 5698 5704 5710 5716 5722 5728 5734 5740 5746 5752 5758 5764 5770 5776 5782 5788 5794 5798 5804 5810 5816 5822 5828 5834 5840 5846 5852 5858 5864 5870 5876 5882 5888 5894 5898 5904 5910 5916 5922 5928 5934 5940 5946 5952 5958 5964 5970 5976 5982 5988 5994 5998 6004 6010 6016 6022 6028 6034 6040 6046 6052 6058 6064 6070 6076 6082 6088 6094 6098 6104 6110 6116 6122 6128 6134 6140 6146 6152 6158 6164 6170 6176 6182 6188 6194 6198 6204 6210 6216 6222 6228 6234 6240 6246 6252 6258 6264 6270 6276 6282 6288 6294 6298 6304 6310 6316 6322 6328 6334 6340 6346 6352 6358 6364 6370 6376 6382 6388 6394 6398 6404 6410 6416 6422 6428 6434 6440 6446 6452 6458 6464 6470 6476 6482 6488 6494 6498 6504 6510 6516 6522 6528 6534 6540 6546 6552 6558 6564 6570 6576 6582 6588 6594 6598 6604 6610 6616 6622 6628 6634 6640 6646 6652 6658 6664 6670 6676 6682 6688 6694 6698 6704 6710 6716 6722 6728 6734 6740 6746 6752 6758 6764 6770 6776 6782 6788 6794 6798 6804 6810 6816 6822 6828 6834 6840 6846 6852 6858 6864 6870 6876 6882 6888 6894 6898 6904 6910 6916 6922 6928 6934 6940 6946 6952 6958 6964 6970 6976 6982 6988 6994 6998 7004 7010 7016 7022 7028 7034 7040 7046 7052 7058 7064 7070 7076 7082 7088 7094 7098 7104 7110 7116 7122 7128 7134 7140 7146 7152 7158 7164 7170 7176 7182 7188 7194 7198 7204 7210 7216 7222 7228 7234 7240 7246 7252 7258 7264 7270 7276 7282 7288 7294 7298 7304 7310 7316 7322 7328 7334 7340 7346 7352 7358 7364 7370 7376 7382 7388 7394 7398 7404 7410 7416 7422 7428 7434 7440 7446 7452 7458 7464 7470 7476 7482 7488 7494 7498 7504 7510 7516 7522 7528 7534 7540 7546 7552 7558 7564 7570 7576 7582 7588 7594 7598 7604 7610 7616 7622 7628 7634 7640 7646 7652 7658 7664 7670 7676 7682 7688 7694 7698 7704 7710 7716 7722 7728 7734 7740 7746 7752 7758 7764 7770 7776 7782 7788 7794 7798 7804 7810 7816 7822 7828 7834 7840 7846 7852 7858 7864 7870 7876 7882 7888 7894 7898 7904 7910 7916 7922 7928 7934 7940 7946 7952 7958 7964 7970 7976 7982 7988 7994 7998 8004 8010 8016 8022 8028 8034 8040 8046 8052 8058 8064 8070 8076 8082 8088 8094 8098 8104 8110 8116 8122 8128 8134 8140 8146 8152 8158 8164 8170 8176 8182 8188 8194 8198 8204 8210 8216 8222 8228 8234 8240 8246 8252 8258 8264 8270 8276 8282 8288 8294 8298 8304 8310 8316 8322 8328 8334 8340 8346 8352 8358 8364 8370 8376 8382 8388 8394 8398 8404 8410 8416 8422 8428 8434 8440 8446 8452 8458 8464 8470 8476 8482 8488 8494 8498 8504 8510 8516 8522 8528 8534 8540 8546 8552 8558 8564 8570 8576 8582 8588 8594 8598 8604 8610 8616 8622 8628 8634 8640 8646 8652 8658 8664 8670 8676 8682 8688 8694 8698 8704 8710 8716 8722 8728 8734 8740 8746 8752 8758 8764 8770 8776 8782 8788 8794 8798 8804 8810 8816 8822 8828 8834 8840 8846 8852 8858 8864 8870 8876 8882 8888 8894 8898 8904 8910 8916 8922 8928 8934 8940 8946 8952 8958 8964 8970 8976 8982 8988 8994 8998 9004 9010 9016 9022 9028 9034 9040 9046 9052 9058 9064 9070 9076 9082 9088 9094 9098 9104 9110 9116 9122 9128 9134 9140 9146 9152 9158 9164 9170 9176 9182 9188 9194 9198 9204 9210 9216 9222 9228 9234 9240 9246 9252 9258 9264 9270 9276 9282 9288 9294 9298 9304 9310 9316 9322 9328 9334 9340 9346 9352 9358 9364 9370 9376 9382 9388 9394 9398 9404 9410 9416 9422 9428 9434 9440 9446 9452 9458 9464 9470 9476 9482 9488 9494 9498 9504 9510 9516 9522 9528 9534 9540 9546 9552 9558 9564 9570 9576 9582 9588 9594 9598 9604 9610 9616 9622 9628 9634 9640 9646 9652 9658 9664 9670 9676 9682 9688 9694 9698 9704 9710 9716 9722 9728 9734 9740 9746 9752 9758 9764 9770 9776 9782 9788 9794 9798 9804 9810 9816 9822 9828 9834 9840 9846 9852 9858 9864 9870 9876 9882 9888 9894 9898 9904 9910 9916 9922 9928 9934 9940 9946 9952 9958 9964 9970 9976 9982 9988 9994 9998

Oy 339 SAELPPLVLMHPKP 351

370 FAEL.PETI.THSKP 382

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Search completed: May 20, 2006, 22:48:27

Job time : 42 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 22:37:51 ; Search time 301 Seconds
(without alignments)
1177.013 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 1973

Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVENTFRQDTIDQQASWDFF 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: UniProt 7.2:*

2: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	1973	100.0	383	2	Q7PMG5_ANOGA	Q7pmg5 anopheles g
2	1973	100.0	383	2	Q95NF3_ANOGA	Q95nf3 anopheles g
3	1515	76.8	381	2	Q9BIG9_9NEOP	Q9big9 ascalaphus
4	1499	76.0	381	1	ARRH_HELV1	P55274 heliothis v
5	1384	70.1	364	1	ARRA_DROME	P15372 drosophila
6	1335	67.7	363	1	ARR1_CALVI	P51486 calliphora
7	1254	63.6	245	2	Q6VPP0_ANOGA	Q6vpp0 anopheles g
8	1219	61.8	269	2	Q5TNW2_ANOGA	Q5tnw2 anopheles g
9	1036	52.5	431	2	Q7Q2V9_ANOGA	Q7q2v9 anopheles g
10	1023	51.8	398	2	Q7Q5Q8_ANOGA	Q7q5q8 anopheles g
11	1002	50.8	470	2	Q9V393_DROME	Q9v393 drosophila
12	993.5	50.4	407	1	ARRH_LOCMI	P32122 locusta mig
13	982.5	49.8	401	1	ARRB_DROME	P19107 drosophila
14	977.5	49.5	401	1	ARRB_DROME	P19108 drosophila
15	953	48.3	390	2	Q5BIJ0_DROME	Q5bij0 drosophila
16	937.5	47.5	400	1	ARRB_CALVI	P51487 calliphora
17	931	47.2	400	1	ARRH_LIMPO	P51484 limulus pol
18	931	47.2	419	2	Q86BW6_HALRO	Q86bw6 halocyathia
19	922.5	46.8	418	2	Q8MYB1_CTOIN	Q8myb1 ciona intes
20	919	46.6	412	2	Q641D8_XENLA	Q641d8 xenopus lae
21	912.5	46.2	410	2	Q4R562_MACFRA	Q4r562 macaca fasc
22	912.5	46.2	410	2	Q8BTJ5_MOUSE	Q8btj5 mus musculus
23	904.5	45.8	418	1	ARRB1_MOUSE	Q8bwg8 mus musculu
24	904.5	45.8	418	2	Q3UH95_MOUSE	Q3uh95 m adult mal
25	903.5	45.8	418	1	ARRB1_BOVIN	P17870 bos taurus
26	903.5	45.8	418	1	ARRB1_RAT	P29066 rattus norv
27	900.5	45.6	418	1	ARRB1_HUMAN	P49407 homo sapien
28	900.5	45.6	418	2	Q2PP20_MOUSE	Q2pp20 homo sapien
29	893	45.3	408	2	Q7T2D2_BRARE	Q7t2d2 brachydano
30	888.5	45.0	435	1	ARRB_CAEEL	P51485 caenorhabdi
31	887	45.0	420	1	ARRB2_BOVIN	P32120 bos taurus

ALIGNMENTS

RESULT 1	Q7PMG5_ANOGA	PRELIMINARY;	PRT;	383 AA.
ID	Q7PMG5_ANOGA			
AC	Q7PMG5_			
DT	15-DEC-2003,	integrated into UniProtKB/Trembl.		
DT	07-DEC-2004,	sequence version 2.		
DT	07-FEB-2006,	entry version 12.		
DE	ENSANGP0000012569.			
GN				
ORFNames=ENSAANGG0000010080;				
OS	Anopheles gambiae str. PEST.			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.			
OX	NCBI_TaxID=180454;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	The Anopheles gambiae re-annotation.";			
RT	"Anopheles gambiae			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=PEST;			
RG	The Anopheles gambiae Sequence Committee;			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.			
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CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC				
DR	EMBL; AAB01008980; EAA13874.3; -; Genomic_DNA.			
DR	GO; GO:0007600; P:sensory perception; IEA.			
DR	GO; GO:0007165; P:signal transduction; IEA.			
DR	InterPro; IPR00698; Arrestin.			
DR	InterPro; IPR01022; Arrestin_C.			
DR	InterPro; IPR011021; Arrestin_N.			
DR	PANTHER; PTHR11792; Arrestin_1.			
DR	Pfam; PF02752; Arrestin_C; 1.			
DR	Pfam; PF00339; Arrestin_N; 1.			
DR	PRINTS; PR00309; ARRESTIN.			
DR	PRODom; PD002099; Arrestin; 2.			
DR	PROSITE; PS00295; Arrestin; 1.			
DR	SEQUENCE; 383 AA; 42809 MW; FA946438592BB53E CRC64;			

Query	Match	100.0%;	Score	1973;	DB	2;	Length	383;	
Best	Local Similarity	100.0%;	Pred.	No.	1.1e-146;				
Matches	383;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
P29066	rattus norvegicus								
P49407	homo sapiens								
Q2pp20	homo sapiens								
Q7t2d2	brachydano								
P51485	caenorhabditis elegans								
P32120	bos taurus								

QY 61 FRYGREEDEVMLNFOKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
 DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS00295; ARRESTINS; 1.
 SQ SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;

Qy 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOQ 180
 DR PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOQ 180
 DR 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOQ 180

Qy 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
 DR 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
 DR 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240

Qy 241 VVLFFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNPKRGIA LDQI KRDQ 300
 DR 241 VVLFFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNPKRGIA LDQI KRDQ 300
 DR 241 VVLFFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNPKRGIA LDQI KRDQ 300

Qy 301 CLASTTLLAQPDQDRAFTGVVIISAVKVKLFLGALGELS AELPFVLMHPKGTKAKVHA 360
 DR 301 CLASTTLLAQPDQDRAFTGVVIISAVKVKLFLGALGELS AELPFVLMHPKGTKAKVHA 360
 DR 301 CLASTTLLAQPDQDRAFTGVVIISAVKVKLFLGALGELS AELPFVLMHPKGTKAKVHA 360

Qy 361 DSQADVETFRQDTIDQQASVDFE 383
 DR 361 DSQADVETFRQDTIDQQASVDFE 383
 DR 361 DSQADVETFRQDTIDQQASVDFE 383

RESULT 2
 Q95NF3_ANOGA PRELIMINARY; PRT; 383 AA.

ID Q95NF3_ANOGA PRELIMINARY; PRT; 383 AA.

AC 01-DEC-2001, integrated into UniProtKB/TremBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Arrestin.

GN Name=Arri;
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
 OC Anophelinae; Anopheles.

NCBI_TaxID=7165;

RN [1] NUCLEOTIDE SEQUENCE.

RC TISSUE=Antennae, and Head;

RX MEDLINE=21680430; PubMed=11822731; DOI=10.1007/s00436-002-0637-0;

RA Ricci I., Santolamazza F., Costantini C., Favia G.;

RT "Molecular characterization and chromosomal mapping of transcripts having tissue-specific expression in the malaria mosquito anophelines gambiae: possible involvement in visual or olfactory processes.";
 RT parasitot. Res. 88:1-8(2002).

RN [2] NUCLEOTIDE SEQUENCE.

RC STRAIN=G3;

RX MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499;

RA Merrill C.E., Riesgo-Escobar J., Pitts R.J., Kafatos F.C.,

RT "Visual arrestsins in olfactory pathways of Drosophila and the malaria vector mosquito Anopheles gambiae.", Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638 (2002).

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DR EMBL; AJ304409; CAC39103.2; -; mRNA.

DR EMBL; AY017417; AAG54081.1; -; mRNA.

DR HSSP; P17870; 1G4M.

DR Ensembl; ENSANGG0000010080; Anopheles gambiae.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR00698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR PANTHER; PTHR11792; Arrestin_1.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS00295; ARRESTINS; 1.
 SQ SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;

Query Match Best Local Similarity 100.0%; Score 1973; DB 2; Length 383;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVNFKVKKKCAPNGKVTLYMGKRDVFHVSGVEPIDI GTVLDDEYIRDNRKVFGQIVCS 60
 DR 1 MVVNFKVKKKCAPNGKVTLYMGKRDVFHVSGVEPIDI GTVLDDEYIRDNRKVFGQIVCS 60

Qy 61 FRYGREEDEVMLNFOKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
 DR 61 FRYGREEDEVMLNFOKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

Qy 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOQ 180
 DR 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOQ 180

Qy 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
 DR 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240

Qy 241 VVLFFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNPKRGIA LDQI KRDQ 300
 DR 241 VVLFFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNPKRGIA LDQI KRDQ 300

Qy 301 CLASTTLLAQPDQDRAFTGVVIISAVKVKLFLGALGELS AELPFVLMHPKGTKAKVHA 360
 DR 301 CLASTTLLAQPDQDRAFTGVVIISAVKVKLFLGALGELS AELPFVLMHPKGTKAKVHA 360

Qy 361 DSQADVETFRQDTIDQQASVDFE 383
 DR 361 DSQADVETFRQDTIDQQASVDFE 383

RESULT 3
 Q9BIG9_9NEOP PRELIMINARY; PRT; 381 AA.

ID Q9BIG9_9NEOP PRELIMINARY; PRT; 381 AA.

AC Q9BIG9_9NEOP PRELIMINARY; PRT; 381 AA.

DT 01-JUN-2001, integrated into UniProtKB/TremBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 17.

DE Arrestin.

GN Name=arri;
 OS Ascalaphus macaronius.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Neuroptera; Ascalaphidae; Ascalaphus.

OX NCBI_TaxID=146496;

RN [1] NUCLEOTIDE SEQUENCE.

RC TISSUE=Head;

RX MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;

RA Bentrop J., Schillo M., Gerdon G., Draslar G., Paulsen R.;"UV-light-dependent binding of a visual arrestin 1 isoform to photoreceptor membranes in a neuropteran (Ascalaphus) compound eye."; FEBS Lett. 493:112-116(2001).

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CC EMBL; AJ303080; CAC36938.1; -; mRNA.

DR HSSP; P17870; 1G4M.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR00698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR PANTHER; PTNR11792; Arrestin_1.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.

10/056, 405

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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DR	PROSITE; PS00295; ARRESTINS; 1.	FT	CHAIN	1	381	Arrestin homolog.
SQ	SEQUENCE 381 AA; 42789 MW; 451DEF465969857D CRC64;	FT				/FTId=PRO 0000205220.
Query Match						
Best Local Similarity	76.8%; Score 1515; DB 2; Length 381;	FT				
Matches 289; Conservative	75.7%; Pred. No. 1.3e-10;	SEQUENCE	381 AA; 42747 MW; 84BB92B1BB3DA573 CRC64;			
Matches 289; Conservative	75.7%; Pred. No. 2.4e-10;					
Mismatches 41; Indels 6; Gaps 4;	72.7%; Pred. No. 2.4e-10;					
Db	1 MVYNFKVKKKCAPNGKVTLYMGKRDVFHVSGVEPIDGIWVLDEYI-RDNRKVFGOTIVC 59	Query Match	76.0%; Score 1499; DB 1; Length 381;			
Db	1 MVANFKVKKKSSPNNGKITTYLGKRDVFHVSGVEPVDGVLILDDDYINOKERKVFGQIVC 60	Best Local Similarity	72.7%; Pred. No. 2.4e-10;			
Qy	60 SFRYGREEDEVNLQGELINFOKECLASEQIYPPEKSDEKEOTKLQERLLKKLGNSNAIPFTENI 119	Mismatches 51; Mismatches 51;				
Db	61 SFRYGREEDEVNLQGELINFOKECLASEQIYPPEKSDEKEOTKLQERLLKKLGNSNAIPFTENI 119	Indels 2; Gaps 2;				
Qy	120 SPNAPSSVTLQGEGDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOG 179	Db	119 PPNAPATITLQPGAEQDGEPGVQYFLKAFVGESDTERPHARSVSMSMQRKQVAPSKQ 178	Qy	61 FRYGREEDEVNLQGELINFOKECLASEQIYPPEKSDEKEOTKLQERLLKKLGNSNAIPFTENI 119	
Qy	180 QQPCTVLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 239	Db	120 SFRYGREEDEVNLQGELINFOKECLASEQIYPPEKSDEKEOTKLQERLLKKLGNSNAIPFTENI 119	Qy	1 MVYNFKVKKKCAPNGKVTLYMGKRDVFHVSGVEPIDGIWVLDEYI-RDNRKVFGOTIVC 60	
Qy	180 QQPCTVLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 239	Db	60 SFRYGREEDEVNLQGELINFOKECLASEQIYPPEKSDEKEOTKLQERLLKKLGNSNAIPFTENI 119	Qy	1 MVYNFKVKKKSSPNNGKITTYLGKRDVFHVSGVEPVDGVLILDDDYINOKERKVFGQIVC 60	
Db	179 RQPCTVVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 238	Db	121 PNAPSSVTLQGEGDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOG 179	Qy	121 PNAPSSVTLQGEGDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOG 179	
Qy	240 DVVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQD 299	Db	120 PGAPGSVILQPGLEDDGEPGVQYVVKIFVGDSIDRSHRRSTVALGIRKQVAPAKGP 179	Qy	181 QPCTVLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 240	
Db	239 DVVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQD 298	Db	180 QPCTVLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 239	Qy	181 QPCTVLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKAMVQQGV 240	
Qy	300 OCLASTTLLAOPDQDRAFTGIVIISAVVKVLFLGALGGELSAELPFVLMHPKPGTKAKVTH 359	Db	241 VVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQD 300	Qy	241 VVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQD 300	
Db	299 TNLASTTLLAOPDQDRAFTGIVIISAVVKVLFLGALGGELSAELPFVLMHPKPGTKAKVTH 357	Db	240 VVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVLHPTLAHNRDKRGIADGOLRSRT 299	Qy	240 VVLFQNGSYRNTVASLETSEGCP1QPGSSLOKVLHPTLAHNRDKRGIADGOLRSRT 299	
Qy	360 ADSQADVETFROPTIDQQASVD 381	Db	301 CLASTTLLAOPDQDRAFTGIVIISAVVKVLFLGALGGELSAELPFVLMHPKPGTKAKVTH 360	Qy	301 CLASTTLLAOPDQDRAFTGIVIISAVVKVLFLGALGGELSAELPFVLMHPKPGTKAKVTH 360	
Db	358 ADSQADVEMFROPTVHD-PDVD 377	Db	300 TLASTTLLDOPDQDRAFTGIVIISAVVKVLFLGALGGELSAELPFVLMHPKREG-RVKMTHA 358	Qy	361 DSQADVETFROPTIDQQASVD 381	
Db	358 ADSQADVEMFROPTVHD-PDVD 377	Db	359 DSQADVEMFROPTVHHQESVE 379	Qy	361 DSQADVETFROPTIDQQASVD 381	
RESULT 4						
ARRH_HELVI	STANDARD; PRT; 381 AA.	ARRH_HELVI	STANDARD; PRT; 381 AA.	ARRH_HELVI	STANDARD; PRT; 381 AA.	
ID	P55274;	ID	P55274;	ID	P55274;	
AC	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.	AC	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.	AC	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.	
DT	01-OCT-1996, sequence version 1.	DT	01-OCT-1996, sequence version 1.	DT	01-OCT-1996, sequence version 1.	
DT	07-FEB-2006, entry version 26.	DT	07-FEB-2006, entry version 26.	DT	07-FEB-2006, entry version 26.	
DE	Arrestin homolog.	DE	Arrestin homolog.	DE	Arrestin homolog.	
OS	Heliothis virescens (Noctuid moth) (Owlet moth).	OS	Heliothis virescens (Noctuid moth) (Owlet moth).	OS	Heliothis virescens (Noctuid moth) (Owlet moth).	
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.	
OX	NCBI_TaxID=7102;	OX	NCBI_TaxID=7102;	OX	NCBI_TaxID=7102;	
RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Antenna;	RC	TISSUE=Antenna;	RC	TISSUE=Antenna;	
RX	MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;	RX	MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;	RX	MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;	
RA	Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae.";	RA	Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae.";	RA	Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae.";	
RT	Cell. Signal. 5:69-80 (1993).	RT	Cell. Signal. 5:69-80 (1993).	RT	Cell. Signal. 5:69-80 (1993).	
RL	-!- SIMILARITY: Belongs to the arrestin family.	RL	-!- SIMILARITY: Belongs to the arrestin family.	RL	-!- SIMILARITY: Belongs to the arrestin family.	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NoDerivs license	CC	Distributed under the Creative Commons Attribution-NoDerivs license	CC	Distributed under the Creative Commons Attribution-NoDerivs license	
CC	InterPro; IPR000698; Arrestin.	CC	InterPro; IPR000698; Arrestin.	CC	InterPro; IPR000698; Arrestin.	
DR	InterPro; IPR011022; Arrestin-C.	DR	InterPro; IPR011022; Arrestin-C.	DR	InterPro; IPR011022; Arrestin-C.	
DR	InterPro; IPR011021; Arrestin-N.	DR	InterPro; IPR011021; Arrestin-N.	DR	InterPro; IPR011021; Arrestin-N.	
DR	PANTHER; PTHR11792; Arrestin-C; 1.	DR	PANTHER; PTHR11792; Arrestin-C; 1.	DR	PANTHER; PTHR11792; Arrestin-C; 1.	
DR	Pfam; PF02752; Arrestin-C; 1.	DR	Pfam; PF02752; Arrestin-C; 1.	DR	Pfam; PF02752; Arrestin-C; 1.	
DR	Pfam; PF00339; Arrestin-N; 1.	DR	Pfam; PF00339; Arrestin-N; 1.	DR	Pfam; PF00339; Arrestin-N; 1.	
DR	PRINTS; PR00309; ARRESTIN.	DR	PRINTS; PR00309; ARRESTIN.	DR	PRINTS; PR00309; ARRESTIN.	
DR	ProDom; PD002099; Arrestin; 2.	DR	ProDom; PD002099; Arrestin; 2.	DR	ProDom; PD002099; Arrestin; 2.	
DR	PROSITE; PS00295; ARRESTINS; 1.	DR	PROSITE; PS00295; ARRESTINS; 1.	DR	PROSITE; PS00295; ARRESTINS; 1.	
KW	Sensory transduction.	KW	Sensory transduction.	KW	Sensory transduction.	
RESULT 5						
ARRA_DROME	STANDARD; PRT; 364 AA.	ARRA_DROME	STANDARD; PRT; 364 AA.	ARRA_DROME	STANDARD; PRT; 364 AA.	
ID	P15372; Q9VJA8;	ID	P15372; Q9VJA8;	ID	P15372; Q9VJA8;	
AC	01-APR-1990, integrated into UniProtKB/Swiss-Prot.	AC	01-APR-1990, integrated into UniProtKB/Swiss-Prot.	AC	01-APR-1990, integrated into UniProtKB/Swiss-Prot.	
DT	01-APR-1990, sequence version 1.	DT	01-APR-1990, sequence version 1.	DT	01-APR-1990, sequence version 1.	
DT	07-FEB-2006, entry version 58.	DT	07-FEB-2006, entry version 58.	DT	07-FEB-2006, entry version 58.	
DE	Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).	DE	Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).	DE	Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).	
GN	Name=Arr1; Synonyms=ARRA; ORFNames=CG5711;	GN	Name=Arr1; Synonyms=ARRA; ORFNames=CG5711;	GN	Name=Arr1; Synonyms=ARRA; ORFNames=CG5711;	
OS	Drosophila melanogaster (Fruit fly);	OS	Drosophila melanogaster (Fruit fly);	OS	Drosophila melanogaster (Fruit fly);	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrdoidea; Drosophilidae; Drosophila.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrdoidea; Drosophilidae; Drosophila.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrdoidea; Drosophilidae; Drosophila.	
RN	NCBI_TaxID=7227;	RN	NCBI_TaxID=7227;	RN	NCBI_TaxID=7227;	
RN	[1] NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.	RN	[1] NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.	RN	[1] NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.	
RX	MEDLINE=90138925; PubMed=1689056;	RX	MEDLINE=90138925; PubMed=1689056;	RX	MEDLINE=90138925; PubMed=1689056;	
RA	Smith D.P., Sheih B.-H., Zuker C.S.; "Isolation and structure of an arrestin gene from Drosophila.";	RA	Smith D.P., Sheih B.-H., Zuker C.S.; "Isolation and structure of an arrestin gene from Drosophila.";	RA	Smith D.P., Sheih B.-H., Zuker C.S.; "Isolation and structure of an arrestin gene from Drosophila.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).	RT	Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).	RT	Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).	
RL	[2]	RL	[2]	RL	[2]	
RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=90138926; PubMed=2105491;	RX	MEDLINE=90138926; PubMed=2105491;	RX	MEDLINE=90138926; PubMed=2105491;	
RA	Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S., Benzer S.;	RA	Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S., Benzer S.;	RA	Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S., Benzer S.;	
RT	"Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";	RT	"Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";	RT	"Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).	RT	Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).	RT	Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).	
RN	[3]	RN	[3]	RN	[3]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=Berkeley;	RC	STRAIN=Berkeley;	RC	STRAIN=Berkeley;	
RT	Medline=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;	RT	Medline=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;	RT	Medline=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;	
RT	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amatadites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	RT	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amatadites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	RT	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amatadites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G., Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh R.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Smith H.O., RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of *Drosophila melanogaster*."; RL Science 287:2185-2195 (2000). [4]

RN GENOME REANNOTATION.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review.," Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). [5]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].

RP STRAIN=Berkeley; TISSUE=Head;

RX MEDLINE=22426066; PubMed=12537569;

RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarini H., Krommiller B., Paclib J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; RA "A *Drosophila* full-length cDNA resource.," Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002). [6]

RP PHOSPHORYLATION.

RX MEDLINE=91282780; PubMed=1905538;

RA Matsumoto H., Yamada T.; RT "Phosrestins I and II: arrestin homologs which undergo differential light-induced phosphorylation in the *Drosophila* photoreceptor *in vivo*," Biochem. Biophys. Res. Commun. 177:1306-1312 (1991). [7]

RA FUNCTION.

RX MEDLINE=93303590; PubMed=8316831;

RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M., Zuker C.S.; RT "Arrestin function in inactivation of G protein-coupled receptor rhodopsin *in vivo*," Science 260:1910-1916 (1993). [8]

RL CC - FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2 proteins are mediators of rhodopsin inactivation and are essential

CC for the termination of the phototransduction cascade.

CC -!- INTERACTION:

CC O9VIM6:CGI10949; NbExp=1; IntAct=EBI-145156, EBI-153699; CC O9VAP2:CGI11881; NbExp=1; IntAct=EBI-145156, EBI-186540; CC O9W3Q2:CGI12155; NbExp=1; IntAct=EBI-145156, EBI-151455; CC O9I7S6:CG3754; NbExp=1; IntAct=EBI-145156, EBI-190361; CC O9VEP0:CG3995; NbExp=1; IntAct=EBI-145156, EBI-160250; CC O9VTH5:CG6175; NbExp=1; IntAct=EBI-145156, EBI-86076; CC O9VHL8:CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350; CC -!- TISSUE SPECIFICITY: Expressed specifically and abundantly in the photoreceptors. Inner and outer segments, and the inner plexiform regions of the retina.

CC -!- PTM: Phosphorylated, but does not undergo light-induced phosphorylation.

CC -!- SIMILARITY: Belongs to the arrestin family.

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CC EMBL; M30177; -; NOT_ANNOTATED_CDS; Genomic_DNA.

CC EMBL; M30140; AAA28380.1; -; Genomic_DNA.

CC EMBL; AE003657; AAF53644.1; -; Genomic_DNA.

DR EMBL; AY061824; AAL27635.1; -; mRNA.

DR PIR; A34867; A34867.

DR HSSP; P17870; 1G4M.

DR IntAct; P15372; -.

DR Ensembl; CG5711; *Drosophila melanogaster*.

DR FlyBase; FBgn000120; Arri1.

DR BioCyc; DMEL-XXX-02:DMEL-XXX-02-009314-MONOMER; -.

DR GO; GO:00055624; C:membrane fraction; IDA.

DR GO; GO:0016028; C:rhabdomere; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0016050; P:metarhodopsin inactivation; IGI.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR PANTRIE; PTHR11792; Arrestin; 1.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.

DR PRODOM; PD002099; Arrestin; 2.

DR PROSITE; PS00295; ARRESTINS; 1.

DR KW Complete proteome; Phosphorylation; Sensory transduction; Vision.

FT CHAIN 1 364 /FTId=PRO_0000205215.

FT SQ SEQUENCE 364 AA; 40771 MW; 0DCC764C4P890FC2 CRC64;

Query Match 70.1%; Score 1384; DB 1; Length 364;

Best Local Similarity 70.3%; Pred. No. 2.6e-100;

Matches 258; Conservative 51; Mismatches 54; Indels 4; Gap 2;

Matches 258; Conservative 51; Mismatches 54; Indels 4; Gap 2;

1 MVYNFKVFKKCAPNGKVLYMGKRDVFUDHVGVEPIDGVVLDDDEVYIRDNRKVFGQIVCS 60

1 MVVNFKVFKKCCSPNMITLYMNRDFVDSVTOEPIDGIVLVLDDEYVRQNKRIFVOLCN 60

61 FRYGREDEVVMGLNFOKEKLCLASEQIYPRPEKSDKEQTKLQERULKKLGNSNAILPTENIS 120

61 FRYGYREDDEMIGLRFOKELTTLVSQLQVCP-POKODIOLTKM0ERLKKLGNSNAYPVFMQMP 119

QY 121 PNAPSSVTLQGEDDNGDPGVSYVVKIFAGESETURTHRSTVTL GIRKIQFAPTKQGQ 180

120 PSSPASVVLQOKASDESOPCGVQYFVKIFTGDSDCDCRSRRSTINL GIRKVOYAPTKQGQ 179

QY 181 QPCTLVRKDMLSPGELELEVTLDKQYLHGERIGVNCIRNNSNKMKVKKIKAMVQOGVD 240

DB 180 QPCTIVVRKDFLSPGELELEVTLDKQYLHGERIGVNCIRNNSNKMKVKKIKAMVQOGVD 239

QY 241 VVLFQNGSYRNTVASLETSEGCP10GSS1QKWMYLTPLSSNKORRGIALDGOIKRQDQ 300

DB 240 WLFLONGQRNTIAFMETSEGCP1NPSS1QKWMYLVPLVANCDRAGIAVEGDIKRKT 299

QY 301 CLASTLILAQPORDAAGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVHA 360

Db	300 ALASTTLIASQDARDAFGITIVSYAVKVFLGALGELCAELPFILMHPKPSRKAQI--	356	Oy	301 CLASTTLAQDQDAGFVIIISYAVKVFLGALGELSAELPFVLMHPKPGTKAKVIA	360
Oy	361 DSQADVE 367		: : : : : : : : : : : : : : : : : :	300 SLASTTLIASQEARDAGFIIVSIVAVKVFLGALGELCAELPFILMHPKPSLKA----	354
Db	357 EAEGSIE 363		: : : : : : : : : : : : : : : : : :		
RESULT 6					
ARR1_CALVI	STANDARD;	PRT; 363 AA.			
ID ARR1_CALVI					
AC P51466;					
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.					
DT 01-OCT-1996, sequence version 1.					
DT 07-FEB-2006, entry version 28.					
DE Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).					
GN Name=ARR1;					
OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).					
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.					
OC NCBI_TaxID=7373;					
RN [1]					
RP NUCLEOTIDE SEQUENCE [mRNA].					
RC TISSUE=Retina;					
RX MEDLINE=95014564; PubMed=7929436;					
RA Planger A., Malicki D., Whitney M., Paulsen R.; "Mechanism of arrestin 2 function in rhabdomeric photoreceptors.", J. Biol. Chem. 269:26969-26975(1994).					
RL !- SIMILARITY: Belongs to the arrestin family.					
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CC Distributed under the Creative Commons Attribution-NoDerivs license					
CC EMBL; X79072; CAA55672.1; -; mRNA.					
DR PIR; A55081; A55081.					
DR HSSP; P17870; 1G4M.					
DR InterPro; IPR00698; Arrestin.					
DR InterPro; IPR011022; Arrestin_C.					
DR InterPro; IPR011021; Arrestin_N.					
DR PANTHER; PTHR11792; Arrestin; 1.					
DR Pfam; PF02752; Arrestin_C; 1.					
DR Pfam; PF00339; Arrestin_N; 1.					
DR PRINTS; PR00309; ARRESTIN.					
DR PRODOM; PD002099; Arrestin; 2.					
DR PROSITE; PS00295; ARRESTINS; 1.					
KW Sensory transduction; vision.					
FT CHAIN 1 363	Phosrestin-2.	/FTId=PRO_0000205214.			
FT SEQUENCE 363 AA; 40680 MW; 7C345D818E46C23B CRC64;					
Query Match 67.7%; Score 1335; DB 1; Length 363;					
Best Local Similarity 67.4%; Pred. No. 1.8e-96;					
Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;					
Qy 1 MWVNFKVKEKCAPNGKVLYMGKRDVFHDVSGVGEPEIDGIVVLDDEYIRDNRKVFQGIVCS 60					
Db 1 MVVNFKIFKKASPNMNVLYMNREFDVSQTQVPEVPGDGVWIDDEYIRQNKFIVQLICN 60					
Qy 61 FRYGRRBEDEVGMGLNFOKEKLCLASEQIYPRPEKSDFKEQTKLQERLLKKLGSSNAIPFTNIS 120					
Db 61 FRYGRRBEDEMIGLRFQKELILVSQPVPE-QKTDIQLTKWQERLKKLGSSNAIPFTNIS 119					
Qy 120 PSSPASVVLQKANDSTQPCGVQYFVKVFAPEFILEMP 119					
Db 181 QPCTLVRKDFMLSPGELELEVTLKQYLHGERIGVNICIRNNSNKMKKKIKAMVQCGVDVLFQNGS 180					
Qy 180 QPCTLVRKDFMLSPGELELEVTLKQYLHGERIGVNICIRNNSNKMKKKIKAMVQCGVDVLFQNGS 179					
Db 181 QPCTLVRKDFMLSPGELELEVTLKQYLHGERIGVNICIRNNSNKMKKKIKAMVQCGVDVLFQNGS 179					
Qy 241 VVLFGONGSYRNTVASLETSEGCPIQPSSLQKVMYLTPLSSNKQRGIALDQIKRQDOCLASTTL 239					
Db 240 VVLFGONGQFRNTIAFAESSEGCPLNPGSSLQKIMLVLPNLAACDRAGIAVEGDVKHKNT 299					
Qy 369 FRQDT 373					

Db	241	FRQDT	245		RESULT 8
O5TNW2_ANOGA				O7Q2V9_ANOGA	PRELIMINARY; PRT; 269 AA.
ID O5TNW2_ANOGA				ID O7Q2V9_ANOGA	PRELIMINARY; PRT; 431 AA.
AC O5TNW2;				AC O7Q2V9;	
DT 07-DEC-2004, integrated into UniProtKB/TREMBL.				DT 15-DEC-2003, integrated into UniProtKB/TREMBL.	
DT 07-DEC-2004, sequence version 1.				DT 15-DEC-2003, sequence version 1.	
DT 07-FEB-2006, entry version 15.				DT 07-MAR-2006, entry version 15.	
DE ENSANGP0000027511 (Fragment).				DE ENSANGP0000004989 (Kurtz arrestin-like protein ArrK) (Fragment).	
GN ORFNames=ENSANGG0000010080;				GN Name=ARRK; ORFNames=ENSANGG0000003863;	
Anopheles gambiae str. PEST.				OS Anopheles gambiae str. PEST.	
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.				OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.	
OX NCBI_TaxID180454;				OC OX NCBI_TaxID=180454;	
RN {1}				RN RN	
RP NUCLEOTIDE SEQUENCE.				RP RP	
RC STRAIN=PEST;				RC RC	
RG The Anopheles gambiae Sequence Committee;				RG RG	
RT "Anopheles gambiae re-annotation.";				RT RT	
RL Submitted (APR-2002) to the EMBL/GenBank/DDJB databases.				RL RL	
RN [2]				RN RN	
RP STRAIN=PEST;				RP RP	
RG The Anopheles gambiae Sequence Committee;				RG RG	
RL Submitted (APR-2004) to the EMBL/GenBank/DDJB databases.				RL RL	
RN [3]				RN RN	
CC NUCLEOTIDE SEQUENCE.				CC CC	
Distributed under the Creative Commons Attribution-NoDerivs License				CC CC	
CC EMBL; AAB0108980; EAL39278.1; -; Genomic_DNA.				CC CC	
GO; GO:0007600; P:sensory perception; IEA.				CC CC	
GO; GO:0001765; P:signal transduction; IEA.				CC CC	
DR InterPro; IPR00698; Arrestin.				CC CC	
DR InterPro; IPR011022; Arrestin_C.				CC CC	
DR InterPro; IPR011021; Arrestin_N.				CC CC	
DR PANTHER; PTHR11792; Arrestin; 1.				CC CC	
DR Pfam; PF02752; Arrestin_C; 1.				CC CC	
DR Pfam; PF00339; Arrestin_N; 1.				CC CC	
DR PRINTS; PR00309; ARRESTIN.				CC CC	
DR PRODOM; PD002099; Arrestin; 2.				CC CC	
DR PROSITE; PS00295; ARRESTINS; 1.				CC CC	
FT NON_TER 1				CC CC	
FT NON_TER 269				CC CC	
SQ SEQUENCE 269 AA; 30553 MW; D45300A28A74F4C0 CRC64;				CC CC	
Query Match Best Local Similarity 61.8%; Score 1219; DB 2; Length 269; Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				CC CC	
Qy 1 MVYNFKVKFKCAPNGKVTLYMGKRDVFHDVSGVEPIDGIWLDEYIRDNRKVFGQIVCS 60				CC CC	
Db 37 MVYNFKVKFKCAPNGKVTLYMGKRDVFHDVSGVEPIDGIWLDEYIRDNRKVFGQIVCS 96				CC CC	
Qy 61 FRYGREEDEWMGLNFQKELCLASEQIYPREKEKSDEQTKLQERLLKKLGNSAIPFTENIS 120				CC CC	
Db 97 FRYGREEDEWMGLNFQKELCLASEQIYPREKEKSDEQTKLQERLLKKLGNSAIPFTENIS 156				CC CC	
Qy 121 PNAPSSVTIQQEDDNGDPGCVSYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180				CC CC	
Db 157 PNAPSSVTIQQEDDNGDPGCVSYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 216				CC CC	
Qy 181 QPCTLVRKDFMLSPGELELEVLTDKQLYLHGERIGVNICIRNNNSNKVKIKKA 233				CC CC	
Db 217 QPCTLVRKDFMLSPGELELEVLTDKQLYLHGERIGVNICIRNNNSNKVKIKKA 269				CC CC	
Query Match Best Local Similarity 52.5%; Score 1036; DB 2; Length 431; Matches 191; Conservative 75; Mismatches 85; Indels 2; Gaps 2;				CC CC	
Qy 6 KVFKKCAPNGKVTLYMGKRDVFHDVSGVEPIDGIWLDEYIRDNRKVFGQIVCSFRYGR 65				CC CC	
Db 7 RVFKKSSSNKGKTVLGYKRDVFHDVHITHVPIDGVVLIDPDYKE-RKVFGHVLAFRYGR 65				CC CC	
Qy 66 EEDEVWGLNFQKELCLASEQIYPREKEKSDEQTKLQERLLKKLGNSAIPFTENISPNA 125				CC CC	
Db 66 EDLIDVLGLTFRKDLYLASEQIYP-PLETDRPLTRIQLERLIRKLGANAYPFYFEVPPHCPA 124				CC CC	
Qy 126 SVTLQQGEDDNGDPGCVSYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQOCPCTL 185				CC CC	
Db 125 SVSLQAPGDTGKPGVGDYELKFAGVFGESQEDKHKRNSVRLAIRKIMYAPSKLGEOPSIE 184				CC CC	
Qy 186 VRKDFMLSPGELELEVLTDKQLYLHGERIGVNICIRNNNSNKVKIKMAQGVWDLFO 245				CC CC	

Db 185 VSKEYIILKPNKTHLEASLDKELYHGEELSLSVNVTANNSSTKVKKIKVSVRQFADICLFS 244
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLUSSNKQRGIALDQIQKRDQCLAST 305
 Db 245 TAQYKCTVAEVESEDGCOVAPGFTLSKVFTLTPLANNKDKWGLALDGQQLKEDTNLASS 304
 Qy 306 TLLAQPDQDRAFTGVIIISYAVKVULFLGALGGELSAELPFVLMPKPGTKAKVI 358
 Db 305 TLIAQPSORENLGIIIVQVKVKLCITPLGGDLVAELPFILEMPKEDDDDEPV 357

RESULT 10
 Q705QB ANOGA PRELIMINARY; PRT; 398 AA.
 ID Q705QB ANOGA
 AC Q705QB_066GU6;
 DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
 DT 07-DEC-2004, sequence version 2.
 DT 07-MAR-2006, entry version 14.
 DE ENSANGP0000020628 (Arrestin 2-like protein Arr2).
 GN Name=ARR2; ORFNames=ENSANGG0000018139;
 OS Anopheles gambiae str. PEST.
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=23159591; PubMed=14986925;
 DOI=10.1046/j.1365-2583.2003.00450.x;
 RA Merrill C.E., Pitts R.J., Zwiebel L.J.;
 RT "Molecular characterization of arrestin family members in the malaria
 vector mosquito, Anopheles gambiae.";
 RL Insect Mol. Biol. 12:641-650(2003).
 CC EMBL; AAAB0108960; EAA10755.2; -; Genomic_DNA.
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 CC GO: GO:007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; Arrestin.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; Arrestins; 1.
 SQ SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;

Query Match 51.8%; Score 1023; DB 2; Length 398;
 Best Local Similarity 52.3%; Pred. No. 7.8e-72; Mismatches 204; Conservative 65; Indels 10; Gaps 7;
 Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

Qy 1 MVVNFKEVKCAPNGKTVLQDFDVKHUSGVVEDIDGIWVUDDEVYIRDNRKVFGQIVCS 60
 1 MVVAVKVKKSAPNGKLTVIGKRDIDHTDYCDBIDGVIVLDEEYL-RGRKVFGOLITT 59

Db 60 VRYGREEDEVMGVFKFSKEMVLTKEQIYPM-ENANMEMTPMQERLVKKGANAFTPTEHP 118
 Qy 121 PNAPSSVTLOQGEDDNGDPCCGVYYVVFAGESETDRTRRSTVILGIRKIQAPTQGQ 180
 Db 119 SMAPSSVTLOQAGEDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTLTIKKIQLQYAPVSR 178
 Qy 181 Q-PCTLVRKDFMLSPGELELEVTLDKQQLYHGERIGVNICIRNNSNKMKVKKAMVQGV 239
 Db 179 RLPSLVLVKSGKFTFSQGKINLLEVTLDRERYHGKTAANIIVTNNSRKTUVKSIKCFVWRC 238

RESULT 11
 Q9V393 DROME PRELIMINARY; PRT; 470 AA.
 ID Q9V393_DROME
 AC Q9V393;
 DT 01-MAY-2000, integrated into UniProtKB/TREMBL.
 DT 07-FEB-2006, sequence version 29.
 DE CG1487-PA (Kurtz arrestin) (LD3108P).
 GN Name=krz; ORFNames=CG1487; Dmel CG1487;
 OS Drosophila melanogaster (Fruit Fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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 OC Ephydriodea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
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 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Preiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 RA de Pablo B., Delchev A., Deng Z., Mayd A.D., Dew I., Dietz S.M.,
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 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,

DR HSSP; P17870; 1G4M.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin; 1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; Arrestin.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Sensory transduction.
 FT CHAIN 1 407 Arrestin homolog
 /FTID=PRO_0000205221.
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 Query Match 50.4%; Score 993.5; DB 1; Length 407;
 Best Local Similarity 52.1%; Pred. No. 1.7e-69;
 Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;
 QY 6 KVFKKCAPNGKTVLYMGKRDVFVHVGVEPIDGIVLDEYIRDNRKVFQGIVCSFRYGR 65
 Db 14 KVFKKTTPNGKTVLYGKFHDHVDPIDGIVWVNDYLR-GRKVFGQIIRRGR 72
 QY 66 EEDEVNGLNFOKECLASQIYPRPEKSDEQTKLQERLLKKGSNAIPFTFNISPNA 125
 Db 73 EDEEVNGLKFTKEMVLAKEDQIVPO-TKEKMETLPIQERLMKKGPNAAFPFTFHPASSP 131
 QY 126 SVTLOOGEDDNGDPGVSYKVKIFAGESETDRTHRSTVTLGIRKIOFAPTQGQQ-PCT 184
 Db 132 SVTLQPGDDQCKPLGVEYSVKTWVGDAEKGHKRSAVTLAIKKLUOXAPTRGRRLPSS 191
 QY 185 LVRKDFMLSPGELELEVTDKOLYLGGERIGVNICRANSNKVNKKRKMVQGGDVWL 244
 Db 192 LVSKGFTFSOKRINKLEVTLDREIYHGKLAANVINNSRKVKNVYVVOHCEVTMV 251
 QY 245 ONGSYRNTVASLETSEGCPIQPGSSLQKWMYLTPLISSNKNKRRGIALDGQIKRODCLAS 304
 Db 252 -NAQFSRHVASLETREGCPITPGASFTKVFYLVPCAASNKDRYGRGIALDGYKLDDVNLAS 310
 QY 305 TLLAQ-PDQDRAFTGVIISYAVKVKLFLGAIGGELSAELPFVIMPKPGT---KAKVTH 359
 Db 311 STLVSEGKNTTDAIGIVISYSLRVKLNCGTLLGELQTDVPPFKLJMPAPGTAEREKAQAI- 369
 RESULT 13
 ARR-B DROME STANDARD; PRT; 401 AA.
 ID P19107; Q9VSN6;
 DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
 DT 24-MAY-2004, sequence version 2.
 DT 07-FEB-2006, entry version 54.
 DE Phosrestin-1 (Phosrestin I) (Arrestin B) (Arrestin-2) (49 kDa)
 DE Arrestin-like protein.
 GN Name=ArrB; Synonyms=ArrB; ORFNames=CG5962;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=90232360; PubMed=2158671;
 RA Yamada T., Takeuchi Y., Kmori N., Kobayashi H., Sakai Y., Hotta Y.,
 RA Matsumoto H.; "A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an
 RT arrestin homolog.", Science 248:483-486 (1990).
 RL [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.",
 RL Science 287:2185-2195 (2000).
 RN [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12533757;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.", Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RP PHOSPHORYLATION, AND PROBABLE FUNCTION.
 RX MEDLINE=91282780; PubMed=1905538;
 RA Matsumoto H., Yamada T.;
 RT "Phosrestins I and II: arrestin homologs which undergo differential
 RT light-induced phosphorylation in the Drosophila photoreceptor in
 RT vivo.", Biochem. Biophys. Res. Commun. 177:1306-1312 (1991).
 RN [5] PHOSPHORYLATION SITE SER-366.
 RP MEDLINE=94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3;
 RA Matsumoto H., Kurien B.T., Takagi Y., Kahn E.S., Kinumi T., Komori N.,
 RA Yamada T., Hayashi F., Isono K., Pak W.L.;
 RT "Phosrestin I undergoes the earliest light-induced phosphorylation by
 RT a calcium/calmodulin-dependent protein kinase in Drosophila
 RT photoreceptors.", Neuron 12:997-1010 (1994).
 RL -!- FUNCTION: Probably plays an important role in the photoreceptor
 RN transduction.
 CC -!- TISSUE SPECIFICITY: Inner and outer segments, and the inner

CC plexiform regions of the retina.
 CC --! PTM: Phosphorylated upon light exposure.
 CC -! SIMILARITY: Belongs to the arrestin family.
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 CC
 DR EMBL; M32141; AAA28833.1; - ; Genomic_DNA.
 DR EMBL; AE003554; AAF50380.1; - ; Genomic_DNA.
 DR PIR; A34856; A34856.
 DR HSSP; P17870; 1G4M.
 DR Ensembl; CG5962; Drosophila melanogaster.
 DR FlyBase; FBgn000121; Arr2.
 DR BioCyc; DMEL-XXX-02:DMEL-XXX-02-015817-MONOMER; - .
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR GO; GO:0016028; C:rhabdomere; IDA.
 DR GO; GO:0005625; C:soluble fraction; IDA.
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 DR GO; GO:0016062; P:adaptation of rhodopsin mediated signaling; IMP.
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 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR Complete proteome; Phosphorylation; Sensory transduction; Vision.
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 FT MOD RES 366 366 /FTId=PRO 0000205217.
 FT VARIANT 109 109 Phosphoserine (by CamK).
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 Best Local Similarity 48.7%; Pred. No. 1.2e-68;
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 Db 60 YRYGREEDEVMGVFKFSKELLICREQIVPM-TNPNNMEMTPMQEKLVRKGNSAYPFTFHP 118
 Qy 121 PNAPSSVTLOQGEDDNGDPCCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 Db 119 PNSPSSVTLOQEGDDNGKPLGVEYTIRAFVGDSEDDROHKRSMSVLVIKKLQYAPLNRGQ 178
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 Db 179 RLPSLVSKGFTFSNGKISLEVTLDREIYHGEKTAATVQVSNNSKSVKSICKFCIVQHT 238
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 Qy 354 ---KAKVIHADSDQADVETFRQDTIDQQASVDF 382
 Db 358 SNAMKKMKSIEQHRNVKGYYQDDDNIVFEDE 389
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 ARRB_DROMI STANDARD; PRT; 401 AA.

AC P19108;
 DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1990, sequence version 1.
 DT 07-FEB-2006, entry version 41.
 DE Phosrestin-1 (Phosrestin I) (Arrestin_B) (Arrestin-2) (49 kDa
 DE arrestin-like protein).
 GN Name=Arr2; Synonyms=ArrB;
 OS Drosophila miranda (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7229;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=S204;
 RX MEDLINE=91016944; PubMed=2216789;
 RA Krishnan R., Ganguly R.;
 RT "Nucleotide sequence of the arrestin-like 49 kd protein gene of
 Drosophila miranda.";
 RL Nucleic Acids Res. 18:5894-5894 (1990).
 CC -! FUNCTION: Undergoes light-induced phosphorylation, probably plays
 an important role in the photoreceptor transduction.
 CC -! TISSUE SPECIFICITY: Inner and outer segments, and the inner
 CC plexiform regions of the retina.
 CC -! SIMILARITY: Belongs to the arrestin family.
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 CC
 DR EMBL; X54084; CAA38019.1; - ; Genomic_DNA.
 DR PIR; S11566; S11566.
 DR HSSP; P17870; 1G4M.
 DR FlyBase; FBgn0012552; Dmir\Arr2.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR Phosphorylation; Sensory transduction; Vision.
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 1 MVVSVKVFKKATPNGKVTFYLGRRDFIDHLYCDPVDPGVIVVEPEYLK-NRKVFGQLA
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 Qy 181 Q-PCTLVKDFMLSPGELELEVTLDKOQLYHLGERIGVNICIRNNSNKMKVKIKAMVQOGV 239
 Db 179 RLPSLVSKGFTFSNGKISLEVTLDREIYHGEKTAATVQVSNNSKSVKSICKFCIVQHT 238
 Qy 240 DVVLFQNGSYRNTVASLETSEGCP1QPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRD 299
 Db 239 EITMV-NAQFSKHKVAQLETKEGCPIPTGANLTKTFYLIPLAANNKDRHGIADGHLDKED 297
 Qy 300 QCLASTLLAQ-PDQRDAFGVIIISYAVKVFLGALGGELSAELPFVLMHPKPGT----- 353

Db 298 VNLAASSTMVQEGKNTGDAAGCIVISYSVRIKLNCGTLGGEMQTDVPFKLLOPAPCTIEKKR 357
 Qy 354 ---KAKVIHADSDQADVETFRQDTIDQQASVDF 382
 Db 358 SNAMKKMKSIEQHRNVKGYYQDDDNIVFEDF 389

Search completed: May 20, 2006, 22:43:02
 Job time : 304 secs

RESULT 15

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 DT 12-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE RH28686P.
 GN Name=Arr2;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephdroioidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkeley;
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celiker S.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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 EMBL; BT021234; AXN33382.1; --; mRNA.
 DR FlyBase; FBgn000121; Arr2.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR SEQUENCE; PS00295; ARRESTIN.
 SQ SEQUENCE 390 AA; 43802 MW; 492250C466C0EEEB CRC64;

Query Match 48.3%; Score 953; DB 2; Length 390;
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 Matches 186; Conservative 71; Mismatches 112; Indels 22; Gaps 6;

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Qy 301 CLASTTLLAQ-PDQDAFGVIIISYAVKVKLFLGALGGELSAELPFLVLMHPRPGT----- 353
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OM protein - protein search, using sw model

Run on: May 20, 2006, 22:52:08 ; Search time 28 Seconds
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 Gapop 10.0 , Gapext 0.5
 Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep: *
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep: *
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep: *
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep: *
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep: *
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep: *
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	907.5	46.0	410	2 US-09-880-137-3
2	903.5	45.8	418	2 US-09-880-137-1
3	897.5	45.5	418	2 US-09-880-137-2
4	885.4	44.9	382	2 US-09-880-137-8
5	885.4	44.9	409	2 US-09-880-137-4
6	880.4	44.6	409	2 US-09-880-137-7
7	853.5	43.3	401	2 US-09-949-016-8383
8	853.5	43.3	401	2 US-09-949-016-8384
9	780.5	39.6	388	2 US-09-880-137-6
10	779.5	39.5	388	2 US-09-880-137-5
11	767.5	38.9	315	2 US-09-949-016-9940
12	316	16.0	197	2 US-09-270-767-58832
13	316	16.0	475	2 US-09-270-767-43475
14	225	11.4	137	2 US-09-270-767-32381
15	225	11.4	137	2 US-09-270-767-47598
16	101	5.1	363	2 US-09-270-767-44161
17	99.5	5.0	600	2 US-09-569-037-4
18	95.5	4.8	1034	2 US-09-543-681A-8172
19	92.5	4.7	1651	1 US-08-447-411-2
20	91.5	4.6	416	2 US-09-007-476-2
21	91	4.6	800	2 US-10-104-047-3534
22	91	4.6	866	2 US-09-949-016-10219
23	89.5	4.5	491	2 US-09-712-363-152
24	89.5	4.5	539	2 US-09-134-000C-43363
25	89.5	4.5	725	2 US-08-425-843-2
26	88	4.5	421	2 US-10-094-749-2860

Result No.	Score	Query Match Length	DB ID	Description
1	907.5	46.0	410	2 US-09-880-137-3
2	903.5	45.8	418	2 US-09-880-137-1
3	897.5	45.5	418	2 US-09-880-137-2
4	885.4	44.9	382	2 US-09-880-137-8
5	885.4	44.9	409	2 US-09-880-137-4
6	880.4	44.6	409	2 US-09-880-137-7
7	853.5	43.3	401	2 US-09-949-016-8383
8	853.5	43.3	401	2 US-09-949-016-8384
9	780.5	39.6	388	2 US-09-880-137-6
10	779.5	39.5	388	2 US-09-880-137-5
11	767.5	38.9	315	2 US-09-949-016-9940
12	316	16.0	197	2 US-09-270-767-58832
13	316	16.0	475	2 US-09-270-767-43475
14	225	11.4	137	2 US-09-270-767-32381
15	225	11.4	137	2 US-09-270-767-47598
16	101	5.1	363	2 US-09-270-767-44161
17	99.5	5.0	600	2 US-09-569-037-4
18	95.5	4.8	1034	2 US-09-543-681A-8172
19	92.5	4.7	1651	1 US-08-447-411-2
20	91.5	4.6	416	2 US-09-007-476-2
21	91	4.6	800	2 US-10-104-047-3534
22	91	4.6	866	2 US-09-949-016-10219
23	89.5	4.5	491	2 US-09-712-363-152
24	89.5	4.5	539	2 US-09-134-000C-43363
25	89.5	4.5	725	2 US-08-425-843-2
26	88	4.5	421	2 US-10-094-749-2860

Result No.	Score	Query Match Length	DB ID	Description
1	907.5	46.0	410	2 US-09-880-137-3
2	903.5	45.8	418	2 US-09-880-137-1
3	897.5	45.5	418	2 US-09-880-137-2
4	885.4	44.9	382	2 US-09-880-137-8
5	885.4	44.9	409	2 US-09-880-137-4
6	880.4	44.6	409	2 US-09-880-137-7
7	853.5	43.3	401	2 US-09-949-016-8383
8	853.5	43.3	401	2 US-09-949-016-8384
9	780.5	39.6	388	2 US-09-880-137-6
10	779.5	39.5	388	2 US-09-880-137-5
11	767.5	38.9	315	2 US-09-949-016-9940
12	316	16.0	197	2 US-09-270-767-58832
13	316	16.0	475	2 US-09-270-767-43475
14	225	11.4	137	2 US-09-270-767-32381
15	225	11.4	137	2 US-09-270-767-47598
16	101	5.1	363	2 US-09-270-767-44161
17	99.5	5.0	600	2 US-09-569-037-4
18	95.5	4.8	1034	2 US-09-543-681A-8172
19	92.5	4.7	1651	1 US-08-447-411-2
20	91.5	4.6	416	2 US-09-007-476-2
21	91	4.6	800	2 US-10-104-047-3534
22	91	4.6	866	2 US-09-949-016-10219
23	89.5	4.5	491	2 US-09-712-363-152
24	89.5	4.5	539	2 US-09-134-000C-43363
25	89.5	4.5	725	2 US-08-425-843-2
26	88	4.5	421	2 US-10-094-749-2860

QY 363 QADVETFRODTID 375 ; SOFTWARE: FastSEQ for Windows Version 4.0
Db 363 PVDTNLIELDTND 375 ; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-2

RESULT 2

US-09-880-137-1
; Sequence 1, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-880-137-1

Query Match Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418;
Best Local Similarity 46.8%; Pred. No. 7.8e-86;
Matches 179; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

QY 6 KVFKKCAGNGKVTLYMGRDFDHDHSGVVEPIDGIVVLDDDEVIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKLTIVLGKRDFFVDHDLVDPDGWVLVLPDEYLUKE-RRVVTLTCAFRYGR 65
QY 66 EEDEVMLNFOKEKLCLASEQIYPRPEKSDKEOTKQERLLKKLGSNAIPFTFNISPNA 125
Db 66 EDLDVGLTRKDLFVANVQSFPAPEDKKPLTRIQLERLIKUGEHAYPFTFEIPPNLPC 125
QY 126 SVTLOQGEDDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185
Db 126 SVTLOQGPEDTGKACGVYDYEVKAFCAENLEEKHKRNNSVRVLRVYQADICLEN 185
QY 186 VRKOFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKIKAMVQQGVDDVLFQ 245
Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNHWHTNNTKTVKKIKISVRQYADICLEN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRGGIALDGQIKRQDQCLAST 305
Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYLTLPFLANNREKRGALDGKLIKEDTNLASS 303
QY 306 TLLAQPDORDAFGVILISAVKVKLF-LGALGGELSA---ELPFVLMHPKPGTK-A 355
Db 304 TLLREGANREILGIIVSVKVKLVESRGGLGDLASSDVAELPFTLMHPKPKEEPPHR 363
QY 356 KVIAHDSQADVETFRODTID 375
Db 364 EVPENETPVDTNLIELDTND 383

RESULT 4

US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-880-137-8

Query Match Best Local Similarity 44.9%; Score 885; DB 2; Length 382;
Best Local Similarity 48.3%; Pred. No. 1.4e-84;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCAGNGKVTLYMGRDFDHDHSGVVEPIDGIVVLDDDEVIRDNRKVFGQIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTIVLGKRDFFVDHDLVDPDGWVLVLPDYLKD-RKVVTLTCAFRYGR 66
QY 66 EEDEVMLNFOKEKLCLASEQIYPRPEKSDKEOTKQERLLKKLGSNAIPFTFNISPNA 125

67 EDLDVVLGLSFRKDLFIA TYQAFPPVNPVRPPTRLQDRLLRKLGQHAPFFFTIPQNLPC 1.26

QY 126 SVTLQOGEDDNGDPCCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 SVTLQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVIRKQFAPEKPGQPSAE 186

QY 186 VRKDFMLSPGELELEVTLDKOLYLGKGERIGVNICIRNNSNKMKKKIKAMVOOGDVVLFO 245
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246

QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMYLTPLLSSNKKRKGIA LDGQIKRQDQCLAST 305
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 247 TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGALDGKLKHEDTNLASS 304

QY 306 TLLAQPQDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 305 TIVKEGANKEVILGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP 349

RESULT 5
US-09-880-137-4

; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-880-137-7

Query Match 44.6%; Score 880; DB 2; Length 409;
Best Local Similarity 48.0%; Pred. No. 5.3e-84; Mismatches 99; Indels 4; Gaps 3;
Matches 166; Conservative 77; Mismatches 99; Indels 4; Gaps 3;

QY 6 KVFKKCAPPNGKVTLYMGKRD FVDHVSGVEPIDGIVLVDDEYIRDNRKVFGQIVCSFRYGR 65
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 8 RVFKKSSPNCNLTVIYLGKDFVMDLPKVDPVGVLVDPDYLKD-RKVFTVLTCAFYGR 66

QY 66 EDEEVWGLNFQKBLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTENISPAPS 125
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 67 EDLDVVLGLSFRKDLFIA TYQAFPPVNPVRPPTRLQDRLLRKLGQHAPFFFTIPQNLPC 126

QY 126 SVTLQOGEDDNGDPCCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 SVTLQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVIEKQFAPEKPGQPSAE 186

QY 186 VRKDFMLSPGELELEVTLDKOLYLGKGERIGVNICIRNNSNKMKKKIKAMVOOGDVVLFO 245
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246

QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMYLTPLLSSNKKRKGIA LDGQIKRQDQCLAST 305
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 247 TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGALDGKLKHEDTNLASS 304

QY 306 TLLAQPQDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 305 TIVKEGANKEVILGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP 349

RESULT 6
US-09-880-137-4

Query Match 44.9%; Score 885; DB 2; Length 409;
Best Local Similarity 48.3%; Pred. No. 1.6e-84;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;
Software: FastSEQ for Windows Version 4.0

QY 6 KVFKKCAPPNGKVTLYMGKRD FVDHVSGVEPIDGIVLVDDEYIRDNRKVFGQIVCSFRYGR 65
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 8 RVFKKSSPNCNLTVIYLGKDFVMDLPKVDPVGVLVDPDYLKD-RKVFTVLTCAFYGR 66

QY 66 EDEEVWGLNFQKBLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTENISPAPS 125
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 67 EDLDVVLGLSFRKDLFIA TYQAFPPVNPVRPPTRLQDRLLRKLGQHAPFFFTIPQNLPC 126

QY 126 SVTLQOGEDDNGDPCCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 SVTLQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVIEKQFAPEKPGQPSAE 186

QY 186 VRKDFMLSPGELELEVTLDKOLYLGKGERIGVNICIRNNSNKMKKKIKAMVOOGDVVLFO 245
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246

QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMYLTPLLSSNKKRKGIA LDGQIKRQDQCLAST 305
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 247 TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGALDGKLKHEDTNLASS 304

QY 306 TLLAQPQDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 305 TIVKEGANKEVILGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP 349

RESULT 7
US-09-949-016-8383

; Sequence 8383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8183

QY 126 SVTLQOGEDDNGDPCCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 SVTLQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVIEKQFAPEKPGQPSAE 186

QY 186 VRKDFMLSPGELELEVTLDKOLYLGKGERIGVNICIRNNSNKMKKKIKAMVOOGDVVLFO 245
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246

QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMYLTPLLSSNKKRKGIA LDGQIKRQDQCLAST 305
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 247 TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGALDGKLKHEDTNLASS 304

QY 306 TLLAQPQDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 305 TIVKEGANKEVILGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP 349

Query Match 43.3%; Score 853.5; DB 2; Length 401;
 Best Local Similarity 46.1%; Pred. No. 3.3e-81; Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5;

Qy 17 VTLVYMGKRDVFUDHVGVEPIDGIVWLDDEYIRDNRKVFGQIVCSFRYGREDEVMLNFO 76
 Db 1 LTVYLGKRDVFUDHIDLVDPGVVLVDPPEYLKE-RRVYVLTCAFRYGRDLDVLGLTR 59

Qy 77 KELCLASEQIYPRPEKSDKEQTKLQERLKKLGSNAIPFTFNIISPNAVSILQOGEDDN 136
 Db 60 KDLFVANVOSFPAPADEKPLTRLQERLKKLGEHAYPFTFEIIPPNLPCSVTLOPGPEDT 119

Qy 137 GDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLSPGE 196
 Db 120 GKACGVDYEVKAFCNAENLEEKHKRNNSVRLVIRKVOYAPERPGPQOPTAETRQFLMSDKP 179

Qy 197 LELEVTLKDQLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDDVLFQNGSYRNTVDSL 256
 Db 180 LHLEASLDKEIYHGEPISVNVHVTNTNKVKKIKISVRQYADICLFTAQYKCPVAME 239

Qy 257 ETSEGCPIOPGSSLQKVMYLTPLSSNKKQRGGTALDGQIKRQDQCLASTTLAQDQDA 316
 Db 240 EADD--TVAPSSTFCKVYTLPFLANNREKGLALLDGKLUKHEDTNLASLLREGANREI 297

Qy 317 FGVIIISYAVVKVLFL--GALGGELSA----ELPFVLMHPKGTK--AKVIHADSQADV 366
 Db 298 LGITIVSYVKVKLUVSRGGGLASSDVAELPFTLMHPKPKEEPHREVPENETPVDT 357

Qy 367 ETFRQDTID 375
 Db 358 NLIEDDTND 366

RESULT 8

US-09-949-016-8384
 ; Sequence 8384, Application US/09949016
 ; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIORITY NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/237, 768
 ; PRIOR FILING DATE: 2000-10-20
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-137-6

RESULT 9

US-09-880-137-6
 ; Sequence 6, Application US/09880137
 ; Patent No. 6640025

GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel
 ; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
 ; PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; FILE REFERENCE: MNI-1-131
 ; CURRENT APPLICATION NUMBER: US/09/880, 137
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: US 60/186, 706
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-137-6

Query Match 39.6%; Score 780.5; DB 2; Length 388;
 Best Local Similarity 42.7%; Pred. No. 1.6e-73; Matches 166; Conservative 79; Mismatches 125; Indels 19; Gaps 7;

Qy 6 KVFKKCAPNGKVTLYMGKRDVFUDHVGVEPIDGIVWLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 3 KVFKKTSSNGKLSIYLGKRDVFUDHVTVEPIDGVVLVDPPEYLK-CRKLFVMLTCAFRYGR 61

Qy 66 EEDEVWMGLNFOKECLASEQIYPRPEKSDK-BOTVLUQERLKKLGSNAIPFTFNIISPNAF 124
 Db 62 DDLEVIGLTFRKDLYQVQLQVPAESSPOGALTVLQERLHLKLDNAVPTLQMVNL 121

Qy 125 SSVTLOQGEDDNGDPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCT 184
 Db 122 CSVTLQPGPEDAGKPGCIDEVKSFCNAENPEETVSKRDYVRLVLRKVQFAPPEAGPGPSA 181

Qy 185 LVRDFMLSPGELELEVTLKDQLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDDVLF 244
 Db 182 QTRIRFFLSSAOPLQOAWMDREVHYHGEPISVNVNSINNCTNKVKKIKISVDOITDWL 241

Qy 245 QNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKKQRGGTALDGQIKRQDQCLAS 304
 Db 242 SLDKYTKTTFIOEFTE--TWAANSSFSQSFAVTPLAASCQKRGGLADGKLUKHEDTNLAS 299

Qy 305 TTLLAQPDQDRAFTGVIISYAVVKVLFL--GALGGELSA----ELPFVLMHPKGTKAV 357
 Db 300 STIRPGMDKELLGILVLSYKVRVNLMSCGGILGDLTASDVGVELPLVLIHPKPSHEA- 358

Qy 358 IHADSQADV--ETFRQDTIDQQASVDFE 383
 Db 359 ---\$SEDIVIEEFTRKGEEESQKAVEAE 383

RESULT 10

US-09-949-016-8384
 ; Sequence 8384, Application US/09949016
 ; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIORITY NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/237, 768
 ; PRIOR FILING DATE: 2000-10-20
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-137-6

Query Match 43.3%; Score 853.5; DB 2; Length 401;
 Best Local Similarity 46.1%; Pred. No. 3.3e-81; Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5;

Qy 17 VTLVYMGKRDVFUDHVGVEPIDGIVWLDDEYIRDNRKVFGQIVCSFRYGREDEVMLNFO 76
 Db 1 LTVYLGKRDVFUDHIDLVDPGVVLVDPPEYLKE-RRVYVLTCAFRYGRDLDVLGLTR 59

Qy 77 KELCLASEQIYPRPEKSDKEQTKLQERLKKLGSNAIPFTFNIISPNAVSILQOGEDDN 136
 Db 60 KDLFVANVOSFPAPADEKPLTRLQERLKKLGEHAYPFTFEIIPPNLPCSVTLOPGPEDT 119

Qy 137 GDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLSPGE 196
 Db 120 GKACGVDYEVKAFCNAENLEEKHKRNNSVRLVIRKVOYAPERPGPQOPTAETRQFLMSDKP 179

US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-5

Query Match 38.9%; Score 767.5; DB 2; Length 315;
Best Local Similarity 48.0%; Pred. No. 2.7e-72;
Matches 145; Conservative 66; Mismatches 88; Indels 3; Gaps 2;

Qy 6 KVFKKCAGNGKVTLYMGKRRDFVDHVSGVEPIDGIVVLDEYIRDNRKVFQQIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTIVLGKRDFFDHLKDPVDPGVVLVDPYLD-KKVFTLCAFRYGR 66

Qy 66 EEDEVMLNFOKEICLASEQIYPRPEKSDK-EQTKLQERLLKKLGSNAIPFTFNISPNA 125
Db 67 EDLVLGLSFRKDLFIATQAFPPVNPPRPPTRQLDRLLRKQAHPPFETIPQNLPC 126

Qy 126 SVTLOQGEDDNGDPGVSYVVKIFAGESETDRTRRSTVTLGIRKIQFAPTKQGQQPCT 185
Db 127 SVTLQPGPEDTGKACGVDFFRAFCAKSLEEKSHKRNSVRLVIRKQFAPEKPGQPOPSA 186

Qy 186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMQQGVDVLFQ 245
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKKIKVSROYADICFS 246

Qy 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPPLSSNKKQRGGIALDGQIKRQDQCLAST 305
Db 247 TAQYKCPVAQLEQDD--QVSPPSSTFCKVYTITPLLSNDREKRGALDGGKUKHEDTNLAS 304

Qy 306 TL 307
Db 305 TM 306

RESULT 11
US-09-949-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9940

Query Match 39.5%; Score 779.5; DB 2; Length 388;
Best Local Similarity 42.4%; Pred. No. 2e-73;
Matches 165; Conservative 80; Mismatches 125; Indels 19; Gaps 7;

Qy 6 KVFKKCAGNGKVTLYMGKRRDFVDHVSGVEPIDGIVVLDEYIRDNRKVFQQIVCSFRYGR 65
Db 3 KVFKKTSNNGKLSIYLGKRDFFDHLKDPVDPGVVLVDPYLD-KKVFTLCAFRYGR 61

Qy 66 EEDEVMLNFOKEICLASEQIYPRPEKSDK-EQTKLQERLLKKLGSNAIPFTFNISPNA 124
Db 62 DDLEVIGLTFRKDLVYQTLQVPAESSSPQGPLTVLQERLHHLGDNAIPFTLQMVNL 121

Qy 125 SVTLOQGEDDNGDPGVSYVVKIFAGESETDRTRRSTVTLGIRKIQFAPTKQGQQPCT 184
Db 122 SVTLQPGPEDTGKACGVDFFRAFCAKSLEEKSHKRNSVRLVIRKQFAPEKPGQPOPSA 181

Qy 185 LVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMQQGVDVLFQ 244
Db 182 OTIRRFLLSAQPLQLOQAMMDOREVHYHGEPISVNVNNCTNKVKKIKISVQDQITDVLY 241

Qy 245 QNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPPLSSNKKQRGGIALDGQIKRQDQCLAST 304
Db 242 SLDKVTKTIVFQEFTE--TVAANSSFSQFAVTPILLAASCQKRGALDGGKUKHEDTNLAS 299

Qy 305 TTLLAQPDQDAFGVIIISYAVKVKLFL--GALGGELSA---ELPFVLMHPKGTKAKV 357
Db 300 STIRRPGMDKELLGILGIVSYKVRVNLMSCGGILGDLTASDVGVELPLVLIHKPSHEA- 358

Qy 358 IHADSOQADV---ETFRQDTIDQQASVDFE 383
Db 359 ---SSEDIVTIEFFTRKGEESQKAVEAE 383

US-09-270-767-58832
; Sequence 58832, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270, 767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58832
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-58832

Query Match 16.0%; Score 316; DB 2; Length 197;
Best Local Similarity 49.6%; Pred. No. 6.6e-25;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

Qy 235 VOOGDVVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPPLSSNKKQRGGIALDGQ 294
Db 2 VRQFADICLFLSTAQYSWAEIESEDGCQVAPGFTLSKVFELCPILLANNDKGWGLALDGQ 61

Qy 295 IKRQDQCLASTTLLAQPDQDAFGVIIISYAVKVKLFLGA--LGGELSAELPFVLMHPKP 351
Db 62 LKHEDTNLASSTLITNPQARESLSLGMVHYKVVKLILLSSPLINGDLVAAELPFETLMHPKP 120

RESULT 13
US-09-270-767-43475
; Sequence 43475, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43475
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43475

Query Match 16.0%; Score 316; DB 2; Length 475;
Best Local Similarity 49.6%; Pred. No. 2.7e-24;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

QY 235 VQOGVDDVVLFONGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSNKQRGIALDQ 294
Db 280 VROFFADICLFSQAQYSWAEIESEDGCQVAPGFTLSKVFECLPANNKDKWGLALDQ 339

QY 295 IKRQDQCLASTTLAQPDQDAFGVIIISYAVKVKLFLGA--LGGBELSAELPFVLMHPKP 351
Db 340 LKHEDTNLASSTLITNPAQRSLGIMVHYKVVKVLLISSPLLINGDLVAELPFTLMHPKP 398

RESULT 14
US-09-270-767-32381
; Sequence 32381, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270, 767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32381
LENGTH: 137
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-32381

Query Match 11.4%; Score 225; DB 2; Length 137;
Best Local Similarity 42.6%; Pred. No. 1.5e-15;
Matches 52; Conservative 26; Mismatches 38; Indels 6; Gaps 4;

QY 6 KVFKKCAPNGKVTLYMGKRDVFVDHVSGVEP--IDGIVVLDDEYIRDNRKVFGQIVCSFRY 63
Db 19 RYVKKTSPNCVLTLYLPTRIT--LTGNNPSVLRGIVVWDPKAQGYR-VYAQLTTFRY 75

QY 64 GREDEEVMLNFOKECLASEQIYPRPEKSDEQ-TKLOERLKKLGSNAIPFTFNISP 122
Db 76 GREDEEVMLRFCEAIMSLHQIWPRLEETPTPESLSPLOQEALMKRLGDGAHPFTLSLSY 135

QY 123 AP 124
Db 136 AP 137

Search completed: May 20, 2006, 22:52:44
Job time : 29 secs

RESULT 15
US-09-270-767-47598
; Sequence 47598, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270, 767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47598

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:03:28 ; Search time 181 Seconds
 (without alignments)
 980.173 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 1973
 Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVENTFRODTIDQQASVDFF 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA Main: *
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep: *
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1973	10.0	383	4 US-10-094-240-2
2	1973	10.0	383	4 US-10-056-405-2
3	1973	10.0	383	5 US-10-954-778-238
4	1384	70.1	364	5 US-10-745-237-18
5	1384	70.1	364	6 US-11-097-143-12000
6	1023	51.8	398	4 US-10-094-240-25
7	1023	51.8	398	5 US-10-954-778-241
8	1002	50.8	470	6 US-11-097-143-1314
9	982.5	49.8	401	4 US-10-094-240-27
10	982.5	49.8	401	6 US-11-097-143-12684
11	907.5	46.0	410	3 US-09-880-137-3
12	907.5	46.0	410	3 US-09-880-137A-3
13	903.5	45.8	418	3 US-09-880-137-1
14	903.5	45.8	418	3 US-09-880-137A-1
15	903.5	45.8	452	4 US-10-038-010-52
16	900.5	45.6	418	4 US-10-043-487-348
17	900.5	45.6	418	5 US-10-745-237-216
18	897.5	45.5	418	3 US-09-880-137-2
19	897.5	45.5	418	3 US-09-880-137A-2
20	890	45.1	369	5 US-10-450-763-43933
21	885	44.9	382	3 US-09-880-137-8
22	885	44.9	382	3 US-09-880-137A-8
23	885	44.9	409	3 US-09-880-137-4
24	885	44.9	409	3 US-09-880-137A-4
25	885	44.9	479	6 US-11-170-123-3
26	885	44.9	492	6 US-11-170-123-4
27	880	44.6	409	3 US-09-880-137-7

ALIGNMENTS

Sequence 7, Appli	28	880	44.6	409	3 US-09-800-137A-7
Sequence 54, Appli	29	869.5	44.1	410	4 US-10-038-010-54
Sequence 6702, Ap	30	865	43.8	454	4 US-10-369-493-6702
Sequence 6, Appli	31	780.5	39.6	388	3 US-09-880-137A-6
Sequence 5, Appli	32	780.5	39.6	388	3 US-09-880-137A-6
Sequence 5, Appli	33	779.5	39.5	388	3 US-09-880-137A-5
Sequence 31, Appli	34	779.5	39.5	388	3 US-09-880-137A-5
Sequence 4673, Ap	35	379.5	19.2	466	4 US-10-722-357-31
Sequence 3639, Ap	36	361.5	18.3	212	4 US-10-106-698-4673
Sequence 45375, A	37	351.5	17.8	456	6 US-11-097-143-3639
Sequence 15, Appli	38	173	8.8	65	3 US-09-864-761-45375
Sequence 23, Appli	39	136.5	6.9	335	6 US-11-097-143-3657
Sequence 40768, A	40	111	5.6	38	3 US-09-864-761-40768
Sequence 16, Appli	41	108.5	5.5	612	5 US-10-945-678-16
Sequence 155, App	42	102	5.2	36946	5 US-10-840-512-155
Sequence 15519, A	43	101.5	5.1	632	5 US-10-945-678-15
Sequence 15519, A	44	100.5	5.1	638	5 US-10-733-969A-23
Sequence 15519, A	45	99.5	5.0	342	6 US-11-097-143-15519

RESULT 1
 US-10-094-240-2

; Sequence 2, Application US/10094240
 ; Publication No. US20030082637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZWIEBEL, LAURENCE J.
 ; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
 ; FILE REFERENCE: N8289
 ; CURRENT APPLICATION NUMBER: US/10/094, 240
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 10/056, 405
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/264, 649
 ; PRIORITY FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Anopheles gambiae
 ; US-10-094-240-2

Query Match 100.0%; Score 1973; DB 4; Length 383;
 Best Local Similarity 100.0%; Pred. No. 6e-176;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVFKKCAPNGKVTLYMGKRDFTDHVSGVPEIDGIWVLDDBEYIRDNRKVFQGIVCS 60
 DQ 1 MVYNFKVFKKCAPNGKVTLYMGKRDFTDHVSGVPEIDGIWVLDDBEYIRDNRKVFQGIVCS 60
 QY 61 FRYGREDEDEVMGLNFOKELCLASEQIYPRPEKSDEQTKLOERLLKKLGSSNAIPFTNIS 120
 DQ 61 FRYGREDEDEVMGLNFOKELCLASEQIYPRPEKSDEQTKLOERLLKKLGSSNAIPFTNIS 120
 QY 121 PNAPSSVTLQOGEDDNGPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 DQ 121 PNAPSSVTLQOGEDDNGPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 QY 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNSNKVMTKIKAMVQGVD 240
 DQ 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNSNKVMTKIKAMVQGVD 240

QY 241 VLFQONGSYRNVTASLETSEGCPPIOPGSSLQKVMYTPLISSNKORRGIAQDGQIKRQDQ 300
 DQ 241 VLFQONGSYRNVTASLETSEGCPPIQPGSSLQKVMYTPLISSNKORRGIAQDGQIKRQDQ 300
 QY 301 CLASTTLAQPDQDRAFTGVIISAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVTHA 360
 DQ 301 CLASTTLAQPDQDRAFTGVIISAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVTHA 360

QY 361 DSQADVENTFRODTIDQQASVDFE 383
Db ||||||| ||||| ||||| ||||| |||||
; Publication No. US2003016601A1
; Sequence 2, Application US/10056405
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: N7841
; CURRENT APPLICATION NUMBER: US/10/056,405
; CURRENT FILING DATE: 2002-01-24
; PRIORITY APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
; US-10-056-405-2

Query Match 100.0%; Score 1973; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-176;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVKKKCAGNGKVTLYMGRDKDFVDHVSGVERPDIQVVLDEYIRDNRKVFGQIVCS 60
Db 1 MVYNFKVKKKCAGNGKVTLYMGRDKDFVDHVSGVERPDIQVVLDEYIRDNRKVFGQIVCS 60
QY 61 FRYGREEDEVMLNFOKECLASSEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
Db 61 FRYGREEDEVMLNFOKECLASSEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
QY 121 PNAPSSVTLOQGEDDNGDPGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 121 PNAPSSVTLOQGEDDNGDPGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
QY 181 QPCTLVRKDFMLSPGELELEVTLKDQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
Db 181 QPCTLVRKDFMLSPGELELEVTLKDQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
QY 241 VVLFQONGSYRNTVASLETSEGCP1OPGSSLQOKVMULTPLLSSNKQRGGIALDGOIKRQDQ 300
Db 241 VVLFQONGSYRNTVASLETSEGCP1OPGSSLQOKVMULTPLLSSNKQRGGIALDGOIKRQDQ 300
QY 301 CLASTILLAQPQDQDAFGVVIISYAVKVKLFLGALGGELSAELPFVLMHPKGTKAKVHA 360
Db 301 CLASTILLAQPQDQDAFGVVIISYAVKVKLFLGALGGELSAELPFVLMHPKGTKAKVHA 360
QY 361 DSQADVENTFRODTIDQQASVDFE 383
Db 361 DSQADVENTFRODTIDQQASVDFE 383

RESULT 4
US-10-745-237-18
; Sequence 18, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P015819WO CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 18
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: AAF53644
; FEATURE:
; OTHER INFORMATION: GI:7298421
; US-10-745-237-18

Query Match 70.1%; Score 1384; DB 5; Length 364;

RESULT 3
US-10-954-778-238
; Sequence 238, Application US/10954778
; Publication No. US20050153368A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
; FILE REFERENCE: N1125
; CURRENT APPLICATION NUMBER: US/10/954,778
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649

Best local Similarity 70.3%; Pred. No. 9.4e-121; Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MVYNFKVKKCAPNGKVTLIMGKRDFFDVHSGVERIDGIWVLDEYIRDNRKVFGQIVCS 60
Db 1 MVYNFKVKKCAPNGKVTLIMGKRDFFDVHSGVERIDGIWVLDEYIRDNRKVFGQIVCS 60
Db 1 MVVNFKVKCSPNNMITLYMNRDFDVSDVTQEPIDGIWVLDEYVRQNKRIFVQLVCN 60

QY 61 FRYGREEDEVMGLNFQKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
Db 61 FRYGREDDEMIGLRFOKELTIVLSQQVC-PQKQDILQTKMQRERILKKLGNSNAYPFVQMP 119

QY 121 PNAPSSVTLQOGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 120 PSSPASVVLQOKASDESOPCGVQYFVKIFTGDSDCDRSHRRSTINLGIRKQYAPTKQG 179

QY 181 QPCTLVKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQGVD 240
Db 180 QPCTLVKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQGVD 239

QY 241 VVLFQNGSYRNTVASLETSEGCPIONPGSSLQKVMYLTPLLSNKORRGIALDQIKRQDQ 300
Db 240 VVLFQNGQFRNTIAFMETSEGCPIONPGSSLQKVMYLTPLLVANCDRAGIAVEGDIKRKT 299

QY 301 CLASTTLLAQPDQDAFGVIIISYAVKVLFIGALGELCAELPFILMHPKPSRKAQL--- 356
Db 300 ALASTTLIASQDARDAGFIIVSYAVKVLFIGALGELCAELPFILMHPKPSRKAQL--- 356

QY 361 DSQADVE 367
Db 357 EAEGSIE 363

RESULT 5
US-11-097-143-12000
; Sequence 12000, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Anopheles gambiae
; US-10-094-240-25

Query Match 51.8%; Score 1023; DB 4; Length 398;
Best Local Similarity 52.3%; Pred. No. 7.5e-87;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

QY 1 MVYNFKVKKCAPNGKVTLIMGKRDFFDVHSGVERIDGIWVLDEYIRDNRKVFGQIVCS 60
Db 1 MVVNFKVKCSPNNMITLYMNRDFDVSDVTQEPIDGIWVLDEYVRQNKRIFVQLVCN 59

QY 61 FRYGREEDEVMGLNFQKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
Db 60 YRYGREDDEMIGLRFOKELTIVLSQQVC-PQKQDILQTKMQRERILKKLGNSNAYPFVQMP 118

QY 121 PNAPSSVTLQOGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 119 SMAPSSVTLQGEDDTGKELPGVEYAKAHVGEDESDKGHKRSAVLTIKLQYAPVSRGR 178

QY 181 Q-PCTLVKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQGVD 239
Db 179 RLPLSLVSKGFTFSQGKINLETVLDRIVYHGEKIKAANNIVVTTNSRKTVRSIKCFVQHC 238

QY 240 DVVLFQNGSYRNTVASLETSEGCPIONPGSSLQKVMYLTPLLSNKORRGIALDQIKRQDQ 299

Query Match 70.1%; Score 1384; DB 6; Length 364;
Best Local Similarity 70.3%; Pred. No. 9.4e-121;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

Db 239 EVTMV-NAQFSKHAISLETREGCPITPGASFTKSFFLVPLASSNKDRRGIALDGHLIKEDD 297
 Qy |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 300 QCLASTTLLAQPD-QRDAFGVVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT--KAK 356
 Qy |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 298 VNLLASSTLISEGKCPSDAMGIVVISYSLRVKLNCGTLLGELQTDVFPKLMNPAPGSVERER 357
 Qy 357 VTHADSOADVENTFRODT---IDQQASVDFE 383
 Db 358 VNALKKMKSIERRHRYENSHYADDDDNIVFE 387

RESULT 7
 US-10-954-778-241
 ; Sequence 241, Application US/10954778
 ; Publication No. US20050153368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZWIEBEL, LAURENCE J.
 ; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
 ; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
 ; FILE REFERENCE: N1125
 ; CURRENT APPLICATION NUMBER: US/10/954,778
 ; CURRENT FILING DATE: 2004-09-30
 ; PRIOR APPLICATION NUMBER: 10/056,405
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/264,649
 ; PRIOR FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: Patentin Ver. 3.3
 ; SEQ ID NO 241
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Anopheles gambiae
 ; US-10-954-778-241

Query Match 51.8%; Score 1023; DB 5; Length 398;
 Best Local Similarity 52.3%; Pred. No. 7.5e-87; Mismatches 111; Indels 10; Gaps 7;
 Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

Qy 1 MVYNFKVKFKCAPNGKVTLYMGKRDVFUDHVSGVEPIDGIVVLDEYIRDNRKVFGQIVCS 60
 Db 1 MVVAVKVKFKSAPNGKLTIVYIGKRDFPHTDYCDPDPGVIVLDEEYL-RGRVFGQLITT 59

Qy 61 FRYGKREDEVMLNFOQKELCLASEQIYPPEKSDKEQTOKLQERLLKKLGSNAIPFTFNIS 120
 Db 60 YRYGKREDEVMLNFOQKELCLASEQIYPPEKSDKEQTOKLQERLLKKLGSNAIPFTFNIS 118

Qy 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOOG 180
 Db 119 SMAPPSSVTLOAGEDDTGKPLGVVEYAIKAHVGEDESDKGHKRSAVTLTIKKLQYAPVSRGR 178

Qy 181 Q-PCTLVRKDFMLSPEGELEVLTDKQLYLHGERIGVNICIRNNSNKMWKKIKAMVQGVVVLFQ 239
 Db 179 RLPSLSVKGFTFSQGKINLAVTLDREIYHGEKIAANIVTNNSRKTVKSIKCFVVOHC 238

Qy 240 DVVLFQNGSYRNTVASLETSEGCPIOPGESSLQKVMYLPLISSNKORRGIAIDGOIKRQD 299
 Db 239 EVTMV-NAQFSKHAISLETREGCPITPGASFTKSFLVPLASSNKDRRGIALDGHLIKEDD 297

Qy 300 QCLASTTLLAQPD-QRDAFGVVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT--KAK 356
 Db 298 VNLLASSTLISEGKCPSDAMGIVVISYSLRVKLNCGTLLGELQTDVFPKLMNPAPGSVERER 357

Qy 357 VTHADSOADVENTFRODT---IDQQASVDFE 383
 Db 358 VNALKKMKSIERRHRYENSHYADDDDNIVFE 387

RESULT 9
 US-10-094-240-27
 ; Sequence 27, Application US/10094240
 ; Publication No. US20030082637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZWIEBEL, LAURENCE J.
 ; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
 ; FILE REFERENCE: N8289
 ; CURRENT APPLICATION NUMBER: US/10/094,240
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 10/056,405
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/264,649

RESULT 9
 US-11-097-143-1314
 ; Sequence 1314, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig

```

; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-094-240-27

Query Match 49.8%; Score 982.5; DB 4; Length 401;
Best Local Similarity 48.7%; Pred. No. 4.8e-83;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;
Db 1 MVVNFKVFKKCAPNGKVTLIMGKRDVFHDVSGVEPIDGIWVLDEYIRDNRKVFGQIVCS 60
Qy 61 FRYGREEDEVMLNPKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNS 120
Db 1 MVVNFKVFKKATPNGKVTFYLGRDFIDHIDYCDPVDGVIWEPDYLK-NRKVFGQIATT 59
Qy 60 YRGREEDEVMGVKFSKELLICREQIVEM-TNPNMEMTPMOKLVRLGSNAYPFTFHFP 118
Db 119 PNSPSSVTIQQEGDDNGKPLGVETIRAFVGDSEDRQHKRSMSVLVIKKLQYAPLNRGQ 178
Qy 121 PNAPSSVTIQQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 179 RLPSLVLVKCGFTFSNGKISLEVTLDREIYHGEKTAATVQVSNNSKSVSIKCFIVQHT 238
Qy 181 Q-PCTLVKDFMLSPGELELEVTLDKOQLYHGERIGVNICIRNNSNKMKVKIKAMVQQGV 239
Db 239 EITMV-NAQFSKHAQLETKBEGCPITPGANLTKTFLYIPLAANNKDRHGIALDGHILKED 297
Qy 240 DVVLFONGSYRNTVASLETSEGCPITOQCSSILOKVMVITPLLSNKQRGIALDQIKRQD 299
Db 300 QCLASTTLLAQ-PDQRDAFGVIIYAVKVKFLGALGGELSAELPFVLMHPKPGT---- 353
Qy 354 ---KAKVIHADSOADVETFRQDTIDQASVDF 382
Db 358 SNAKKMKSIEQHHRNVKGYYQDDDDNIVFEDF 389
Db 358 SNAKKMKSIEQHHRNVKGYYQDDDDNIVFEDF 389

RESULT 10
US-11-097-143-12684
; Sequence 12684, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-3

Query Match 46.0%; Score 907.5; DB 3; Length 410;
Best Local Similarity 47.2%; Pred. No. 5.3e-76;
Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;
Db 6 KVFKKCAPNGKVTLIMGKRDVFHDVSGVEPIDGIWVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKUTVYLGKRDVFHDIDLVDPDVGLVLPDEYKLE-RRVYTILCAFRYGR 65
Qy 66 EDEVMGLNPKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNSPNAPS 125
Db 66 EDLVLGLTRKDFVANVOSFPPAPEDKKPLTRLQERLIKLGHEAYPFTFEIPPNLPC 125
Qy 126 SVTLQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQPC 185

; SEQ ID NO 12684
; LENGTH: 401
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-12684

Query Match 49.8%; Score 982.5; DB 6; Length 401;
Best Local Similarity 48.7%; Pred. No. 4.8e-83;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;
Db 1 MVVNFKVFKKCAPNGKVTLIMGKRDVFHDVSGVEPIDGIWVLDEYIRDNRKVFGQIVCS 60
Qy 61 FRYGREEDEVMLNPKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNS 120
Db 60 YRGREEDEVMGVKFSKELLICREQIVEM-TNPNMEMTPMOKLVRLGSNAYPFTFHFP 118
Db 119 PNSPSSVTIQQEGDDNGKPLGVETIRAFVGDSEDRQHKRSMSVLVIKKLQYAPLNRGQ 178
Qy 121 PNAPSSVTIQQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
Db 179 RLPSLVLVKCGFTFSNGKISLEVTLDREIYHGEKTAATVQVSNNSKSVSIKCFIVQHT 238
Qy 240 DVVLFONGSYRNTVASLETSEGCPITOQCSSILOKVMVITPLLSNKQRGIALDQIKRQD 299
Db 239 EITMV-NAQFSKHAQLETKBEGCPITPGANLTKTFLYIPLAANNKDRHGIALDGHILKED 297
Qy 300 QCLASTTLLAQ-PDQRDAFGVIIYAVKVKFLGALGGELSAELPFVLMHPKPGT---- 353
Db 298 VNLAASSTMVQEGKSTGDACGIVISYSVRIKUNCGTLLGEMOTDVFPLQOPAPGTIEKKR 357
Qy 354 ---KAKVIHADSOADVETFRQDTIDQASVDF 382
Db 358 SNAKKMKSIEQHHRNVKGYYQDDDDNIVFEDF 389

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RESULT 12
US-09-800-137A-3

; Sequence 3, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIORITY APPLICATION NUMBER: US 60/186, 706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bob taurus
; US-09-880-137-1

Query Match 45.8%; Score 903.5; DB 3; Length 418;
Best Local Similarity 47.1%; Pred. No. 1.3e-75; Mismatches 112; Indels 13; Gaps 5;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAGNGKVTLYMGKRRDFDVHSVGSVERIDGIVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKLTLYLGKRRDFVDHIDLIVEPDGVWLVDPPEYKE-RRVYVTLCAFRYGR 65

QY 66 EEDEVVMGLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPAPS 125
Db 66 EDLIVLGLTFRKDLFVANVQSFPAPDKPLTRIQLRERLIKLGHEAYPFTFEIPPNLPC 125

QY 126 SVTLQQGEDDNGDPCGVSYVKIFAGBESETDRRSTVTLGIRKIQFAPTKQGQQPCTL 185
Db 126 SVTLQPGPEDTGKACGVYDEVKAFCAEENLEEKIHKRNSVRLVIRKVOYAPERPGPOPTAE 185

QY 186 VRKDFMLSPGELELEVTDKOLYLGERIGNICIRNNSNKMKIKAMVQGQDVLFQ 245
Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVHVNNTNKTKKIKISVRQYADICLN 245

QY 66 EEDEVVMGLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPAPS 125
Db 66 EDLIVLGLTFRKDLFVANVQSFPAPDKPLTRIQLRERLIKLGHEAYPFTFEIPPNLPC 125

QY 126 SVTLQQGEDDNGDPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTL 185
Db 126 SVTLQPGPEDTGKACGVYDEVKAFCAEENLEEKIHKRNSVRLVIRKVOYAPERPGPOPTAE 185

QY 306 TLLAQPDQRDAFGVIIISYAVKVKLFLGALGGELSAELPFVLMHPPKGTK--AKVHADS 362
Db 304 TLLREGANREILGIIVSYVKVKL-VERSGGDVAVELPFTLMHPPKKEEPPHREVNET 362

QY 363 QADVETFRQDTID 375
Db 363 PVDTNLIELDTND 375

RESULT 13
US-09-880-137-1

; Sequence 1, Application US/09880137
; Patent No. US20031295A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIORITY APPLICATION NUMBER: US 60/186, 706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bob taurus
; US-09-880-137-1

Query Match 45.8%; Score 903.5; DB 3; Length 418;
Best Local Similarity 47.1%; Pred. No. 1.3e-75; Mismatches 112; Indels 13; Gaps 5;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAGNGKVTLYMGKRRDFDVHSVGSVERIDGIVLDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNKGKLTLYLGKRRDFVDHIDLIVEPDGVWLVDPPEYKE-RRVYVTLCAFRYGR 65

QY 66 EEDEVVMGLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPAPS 125
Db 66 EDLIVLGLTFRKDLFVANVQSFPAPDKPLTRIQLRERLIKLGHEAYPFTFEIPPNLPC 125

QY 126 SVTLQQGEDDNGDPCGVSYVKIFAGBESETDRRSTVTLGIRKIQFAPTKQGQQPCTL 185
Db 126 SVTLQPGPEDTGKACGVYDEVKAFCAEENLEEKIHKRNSVRLVIRKVOYAPERPGPOPTAE 185

QY 186 VRKDFMLSPGELELEVTDKOLYLGERIGNICIRNNSNKMKIKAMVQGQDVLFQ 245
Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVHVNNTNKTKKIKISVRQYADICLN 245

QY 306 TLLAQPDQRDAFGVIIISYAVKVKLFLGALGGELSAELPFVLMHPPKGTK--AKVHADS 362
Db 304 TLLREGANREILGIIVSYVKVKL-VERSGGDVAVELPFTLMHPPKKEEPPHREVNET 362

QY 363 QADVETFRQDTID 375
Db 363 PVDTNLIELDTND 375

RESULT 14
US-09-800-137A-1

; Sequence 1, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800, 137A
; CURRENT FILING DATE: 2001-03-05
; PRIORITY APPLICATION NUMBER: US 60/186, 706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT

; ORGANISM: Bos taurus
; US-09-800-137A-1

Query Match 45.8%; Score 903.5; DB 3; Length 418;
Best Local Similarity 47.1%; Pred. No. 1.3e-75;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDFFDHHVGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNGLTVLGLKRDFFDHDILIVEPVDGVLVDPEYKE-RRVYVLTCAFRYGR 65

QY 66 EDEVMGLNFOKECLASEQTYPREPKSDKEQTKLQERLKKLGSNAIPFTFNISPNA 125
Db 66 EDLDVNLGLTFRKDLFVANVOSFPAPPADEKKPLTRQLQERLIKKGESRQYADICLNF 125

QY 126 SVTLQGEDDNGDPGCVSYVKFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTL 185
Db 126 SVTLQPGPEDTGKACCGVDEVKAFCAEENLEEKIHKRNNSVRLVIRKVOYAPERPGPQPTAE 185

QY 186 VRKFMLSPGELELEVTLDKOLYLHGERIGVNICRNNNSNKMKIKAMVQGVDVLFQ 245
Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVHTNTKTVKKIKISVRQYADICLNF 245

QY 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLLSNKQRGIALDGQIKRQDQCLAST 305
Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYLTLPFLANNREKRGGLALDGKLUKHEDTNLASS 303

QY 246 TLLAQPDORDAFGVILSYAVKVKLFL--GALGGELSA----ELPFVLMHPPKGTK--A 355
Db 304 TLLREGANREIILGIIVSYKVVKLVVSRGGGLGDLASSDVAVELPFTIMHPKPKEEPPHR 363

QY 356 KVIHADSQADVETFRQDTID 375
Db 364 EVPEHETPVDTNLIELDTND 383

RESULT 15
US-10-038-010-52
; Sequence 52, Application US/10038010
; Publication No. US20030040089A1

GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 452
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta Arrestin 1
LOCATION: (1).-(452)
OTHER INFORMATION:
US-10-038-010-52

Query Match 45.8%; Score 903.5; DB 4; Length 452;
Best Local Similarity 47.1%; Pred. No. 1.5e-75;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDFFDHHVGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65
Db 7 RVFKKASPNGLTVLGLKRDFFDHDILIVEPVDGVLVDPEYKE-RRVYVLTCAFRYGR 65

QY 66 EDEVMGLNFOKECLASEQTYPREPKSDKEQTKLQERLKKLGSNAIPFTFNISPNA 125
Db 66 EDLDVNLGLTFRKDLFVANVOSFPAPPADEKKPLTRQLQERLIKKGESRQYADICLNF 125

Search completed: May 20, 2006, 23:06:38
Job time : 182 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:03:38 ; Search time 11 Seconds
(without alignments)
74.376 Million cell updates/sec

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Perfect score: 1973
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New: *
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	44.9	409	6 US-10-505-928-173	Sequence 173, APP
2	81.5	4.1	862	6 US-10-511-937-2974	Sequence 2974, APP
3	80	4.1	800	6 US-10-196-749-478	Sequence 478, APP
4	77.5	3.9	1212	6 US-10-505-928-201	Sequence 201, APP
5	77	3.9	282	7 US-11-251-466-46	Sequence 46, APP
6	77	3.9	282	7 US-11-264-784-72	Sequence 72, APP
7	75.5	3.8	893	6 US-10-505-928-733	Sequence 733, APP
8	74.5	3.8	299	6 US-10-196-749-164	Sequence 164, APP
9	74.5	3.8	708	7 US-11-170-482-16	Sequence 16, APP
10	73	3.7	763	6 US-10-505-928-304	Sequence 304, APP
11	72.5	3.7	806	7 US-11-251-465-22	Sequence 22, APP
12	72.5	3.7	1075	6 US-10-322-836-48	Sequence 48, APP
13	72.5	3.7	2215	6 US-10-505-928-310	Sequence 310, APP
14	71	3.6	798	6 US-10-511-937-2451	Sequence 2451, APP
15	71	3.6	871	7 US-11-316-132-1	Sequence 1, APP
16	71	3.6	313	6 US-10-505-928-325	Sequence 325, APP
17	70.5	3.6	1809	6 US-10-559-415-190	Sequence 190, APP
18	70.5	3.6	1919	6 US-10-559-415-2	Sequence 245, APP
19	70	3.5	301	7 US-11-101-316-18	Sequence 18, APP
20	69	3.5	870	7 US-11-316-132-2	Sequence 2, APP
21	68.5	3.5	709	7 US-11-170-482-14	Sequence 14, APP
22	67.5	3.4	318	7 US-11-106-014-42	Sequence 42, APP
23	67.5	3.4	729	7 US-11-312-958-64	Sequence 64, APP
24	67.5	3.4	1443	6 US-10-505-928-720	Sequence 720, APP
25	67	3.4	725	6 US-10-370-959-128	Sequence 128, APP

Sequence 135, APP
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Sequence 513, APP
Sequence 8, APP
Sequence 363, APP
Sequence 31, APP
Sequence 75, APP
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Sequence 2463, APP
Sequence 357, APP
Sequence 123, APP
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Sequence 259, APP
Sequence 66, APP
Sequence 2597, APP
Sequence 2992, APP
Sequence 30, APP
Sequence 35, APP

RESULT 1
US-10-505-928-173
; Sequence 173, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIORITY FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 173
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-173

ALIGNMENTS

Query Match Best Local Similarity 44.9%; Score 885; DB 6; Length 409;
Matches 167; Conservativeness 48.3%; Pred. No. 1.5e-90; Indels 98; Gaps 3;
QY 6 KVFKKCAPNGKVTLYMGKRDFFDHWGSGVEPIDGIVVLDDERYIRDRNPKVFGOIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTVLGKRDFFDHWGSGVEPIDGIVVLDDERYIRDRNPKVFGOIVCSFRYGR 66
QY 66 EEDEVMLNFOKBLCLASEQIYRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPNA 125
Db 67 EDLVLGLSFRKDLFIATYQAFFPVNPFRPPTRLQDRDLRKIGOHAAFFFTIPONLPC 126
QY 126 SVTLOQGEDDNGDPCCGVSYVVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQQPCTL 185
Db 127 SVTLQPGPDEDTGKACGVDFFETRAFCAKSLBEKSKRNSVRLVIRKVQFABEKGPQPSAE 186
QY 186 VRKDFMLSPGPELELBVTDKOLYLGERIGVNICIRNNSNKMKKKIKAMVQGVPWLFQ 245
Db 187 TTRFLMLSDRSILHEASLDKELYXHGEPLNVNVTNNNSTKTVKKIKVSQRYADICLS 246
QY 246 NGSYRNTVASLETSEGCPIQPCSSLQKVMYLTPLISSNPKQRGIALDGOKRQDCLAST 305
Db 247 TAQYKCPVAQLEQDD-QWSPSSTFCKVYTITPLISDNREKRGLADGKLUKHEDTNASS 304
QY 306 TLLAQPDQRDAFGVIIISYAVKVLFGLGGELSAELPFVLMHPKP 351
Db 305 TIVKEGANKEVVLGILVSYRVKVKLV-SRGGDVSELVLPFVLMHPKP 349

RESULT 2
 US-10-511-937-2974
 Sequence 2974, Application US/10511937
 Publication No. US20060088836A1
 GENERAL INFORMATION:
 APPLICANT: EXPRESSION DIAGNOSTICS, INC.
 APPLICANT: Wohlgemuth, Jay
 APPLICANT: Fry, Kirk
 APPLICANT: Woodward, Robert
 APPLICANT: LY, Ngoc
 APPLICANT: Prentice, James
 APPLICANT: Morris, MacDonald
 APPLICANT: Rosenberg, Steven
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
 TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
 FILE REFERENCE: 50661200104
 CURRENT APPLICATION NUMBER: US/10/511, 937
 CURRENT FILING DATE: 2004-10-19
 PRIOR APPLICATION NUMBER: PCT/US2003/012946
 PRIOR FILING DATE: 2003-04-24
 PRIOR APPLICATION NUMBER: US 10/131, 831
 PRIOR FILING DATE: 2002-04-24
 PRIOR APPLICATION NUMBER: US 10/325, 899
 NUMBER OF SEQ ID NOS: 3117
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2974
 LENGTH: 862
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-511-937-2974

Query Match 4.1%; Score 81.5; DB 6; Length 862;
 Best Local Similarity 20.6%; Pred. No. 1;
 Matches 60; Conservative 51; Mismatches 129; Indels 51; Gaps 13;

Qy 22 GKRDFDVHVGVEPIDGIVVLDEY---IRDNRKVFQOIVCSFRYGREREDEVMLN-- 74
 Db 525 GDRGSQEHVDSQEKAP---ETDDSDSDVDCHSNQEDTG---CKFRLPQPTNLATPNTR 578

Qy 75 FQKELCLASEQIYPRPEKSDEKQTKLQERLLKKLGSNAIPFTFNISPNSVTL-QQGE 133
 Db 579 FKKEELSSDICQKLUNT-QDMSASQDVAVKINKKVVLDFSMSSLAKRKKQLHHEAQ 637

Qy 134 DDNGDPCCGVSYWKIFAGESETDRTHRSTVT-----LGIRKIQFAPTKQSG--- 180
 Db 638 QSEGEQNYRKFRAKICPGENQAEDLERKEISKTMFAEMETIGOFNLGFITTKLNEDIFI 697

Qy 181 --OPCTLVRKDFMLSPGELELEVTLDKOLYLHGERI---GVNICIRNNSNKVKIKAM 234
 Db 698 VDQHATDEKYNFEM-----LOQHTVLOGQRLIAPIOTNLNTAVNEA-VLIENLEIF 746

Qy 235 VQQGVDVLFQNG--SYRNTVASLETSEGCPIQPGSSLQKVMYLTPLISSN 283
 Db 747 RKNGFDFVIDENAIVTERAKLISLPTSKNWTFGP---QDVDELIFMLSDS 793

RESULT 3
 US-10-196-749-478
 Sequence 478, Application US/10196749
 Publication No. US20060094864A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Wattanabe, Colin K.
 APPLICANT: Wood, William I.

Query Match 4.1%; Score 80; DB 6; Length 800;
 Best Local Similarity 19.6%; Pred. No. 1.3;
 Matches 94; Conservative 69; Mismatches 167; Indels 150; Gaps 25;

Qy 9 KKCAPNGKVTLY-----MCKKRDFDVHVGVEPIDGIVVLDEYIRDNRKV 53
 Db 94 KLCPGPKEPCMLYFOILMDDPFQIYRAELRVRDINDHAPVFQDKETVLKISENTAEGT--- 150

Qy 54 FGQIVCSFRYGREREDEVMLN-----FQKELCLASE-QIYPR---PEKSDEKQ 97
 Db 151 -----AFRLERAQDPDGGLNGNQYNTISPNSFFFHINISGGDEGMIPVELVDKALDR 204

Qy 98 -----TKLQERLLKKLGSNAIPF-TFNISPNS-SVTLQQGEDDNGDPGCVSYVK 147
 Db 205 QGELSLTLTALDGGSPSRSGTSTVRIVLVDNDNAPOFAQALYETQAPENSPIGF-LIVK 263

Qy 148 IFAGESETDRTHRSTVTLGIRKIQFAPTKOGOOPCILVRKDFMLSP--GBELEBLTDK 205
 Db 264 VWAEDDVD-----SGVNAEVSVSFADSEN-----IRTTEQINPESGEIFLRELLDY 309

Qy 206 QLYLHGERIGVNICIRNNSNKVKIKAMVQQGVDV-----VLFQN----GSR 250
 Db 310 ELV-----NSYKI--NIQAMDGGGLSARCRVLCVLEVLDTNPPPELIVSSFS 353

Qy 251 NTVASLETSEGCP-----QPGSSLQKVMYLTP---LSSNKQRGGI----ALDG 293
 Db 354 NSVA--ENSPEPTPLAVFKINDRDSGENGKMCYIQENLPFLKPSVENFYILITEGALDR 411

Qy 294 QIKRQDQCLASTILLAQPQDQDAFGVII-----SYAVVK-----LFTG 332
 Db 412 EIRAEYNITITVTDLGTPRLKTEHNITIVLSDVNNDNAPAFTOITSYLVRENNSPALHG 471

Qy 333 ALGGE-----LSAELPFVLMHPK---PGTAKVTHADSQADVETFRQDTIDQQASVDFE 383
 Db 472 SVSATDRDSGNTAQVTYSLPPQDPHILPLASLVSINADNG--HLFALRSLDYEAQFE 528

RESULT 4
 US-10-505-928-201

; Sequence 201, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIORITY APPLICATION NUMBER: US 60/363, 019
; PRIORITY FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 201
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-201

Query Match 3.9%; Score 77.5; DB 6; Length 1212;
Best Local Similarity 20.8%; Pred. No. 5.2; Mismatches 152; Indels 79; Gaps 17;
Matches 74; Conservative 50; Mismatches 152; Indels 79; Gaps 17;

Qy 56 QIVCFSFRYGRREE-DEVMGLINFOKEKELCLASEQIYPRPREKSDKEQTOKLQERLJKLGNSNAP 114
Db 404 QIKQEFRRGTESLDHLAGLSHYH-ADTSYRHFPEKSEKYSISRLTLEQAKQLPA-AIL 461

Qy 115 FTTFN-----ISPNAFSSVTLQQGEDDNGDPGCVSYV---KIFAGESETDRTHRRST 163
Db 462 YQKQSKHKKSLIDPKMSKFSPQESRDLERD--YSSYMTSSTSSIGGTSRRL-LQDD 517

Qy 164 VTLGIRK----IQFAPTKQGQQPCTL---VRKDFMLSPGEBLELEVTLDKOLYHGER- 213
Db 518 ITFGGLRKNTDQKFMGSLLGTGLTGNTIRS-----ALQDEADKP-YSSGSR 567

Qy 214 -----IGNVICIRNNSNKMKVKKIKAMVQGVEDWLFONGSYRNTVASLETS-EGCPI 264
Db 568 PSSRPSSVYGLDLSIKRDSSSSLRLKAOEAEALDV-----SFSHASSARTKPTSLPI 621

Qy 265 QPGSSLQKVMYLTPPLSSNKQRG-IALDQKIKRQDQCLASTTLLAQPDQDRAFTGVILSY 323
Db 622 SQSRG-----RIPVAQNSEEESPLSPVGQPMGMARAAGPLIPPIASADRQDFG---- 670

Qy 324 AVVKVLFLGAGGELSAELPFVLMHPKPGTKAKVHADSQADVENTFROTDQQA 378
Db 671 -----SSHSLPEVOQHMREBESRTRGYDRIAFIMDDFOHAMSDSEA 711

RESULT 5
US-11-251-466-46
; Sequence 46, Application US/11251466
; Publication No. US20060094090A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company
; APPLICANT: Xue, Zhixiong
; APPLICANT: Damude, Howard Glenn
; TITLE OF INVENTION: A MORTIERELLA ALPINA LYSOPHOSPHATIC ACID ACYLTRANSFERASE
; TITLE OF INVENTION: HOMOLOG FOR ALTERATION OF POLYUNSATURATED FATTY ACIDS AND OIL
; TITLE OF INVENTION: CONTENT IN OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2793 USNA
; CURRENT APPLICATION NUMBER: US/11/251, 466
; CURRENT FILING DATE: 2005-10-14
; PRIORITY APPLICATION NUMBER: US 60/624812
; PRIORITY FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 46
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Yarrowia lipolytica
; US-11-251-466-46

Query Match 3.9%; Score 77; DB 7; Length 282;
Best Local Similarity 24.8%; Pred. No. 0.49; Mismatches 29; Indels 77; Gaps 14;
Matches 58; Conservative 29; Mismatches 77; Indels 70; Gaps 14;

Qy 144 YYVKIFAGESETDRTHRRSTVTLGI--RKIOFAP-----TKOGQOPCTLVRKDFMLS 193
Db 53 YSVRIFLGISIKRS-RQVTGTAQDASKIQVANTTKPIDDITKHLPRPCILSN---H 107

Qy 194 PGEEL-----EVTLDKOLY--LHGERIGVNICI--RNNSNKNMKVKKIKAMVQ 236
Db 108 QNEMDILVLGRIFPOYCSTAKKALKWYPLLGQFMAISGTTFLDRKDRTSVQTLGGAVK 167

Qy 237 -----QGVDMYLONG--SYRNTVASLETSEG---PIOPGSSLQKVMYLTPLSSN 283
Db 168 TIQSGNGKGQSVMFPECTRSYSKDVGIMPFKKGCFHLAVQSGAP-----IVPVVQN 221

Qy 284 KQR-----RGIALDGQI-----KRQD---OCLASTTLLAQPDQDRAFTGVILSY 318
Db 222 TSRMFSGRKGKDAGEILVDVLSPPIETKGLDASNVNDALMATTYKAMCETADQIG 275

RESULT 6
US-11-264-784-72
; Sequence 72, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264, 784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 72
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Yarrowia lipolytica
; US-11-264-784-72

Query Match 3.9%; Score 77; DB 7; Length 282;
Best Local Similarity 24.8%; Pred. No. 0.49; Mismatches 29; Indels 77; Gaps 14;
Matches 58; Conservative 29; Mismatches 77; Indels 70; Gaps 14;

Qy 144 YYVKIFAGESETDRTHRRSTVTLGI--RKIOFAP-----TKOGQOPCTLVRKDFMLS 193
Db 53 YSVRIFLGISIKRS-RQVTGTAQDASKIQVANTTKPIDDITKHLPRPCILSN---H 107

Qy 194 PGEEL-----EVTLDKOLY--LHGERIGVNICI--RNNSNKNMKVKKIKAMVQ 236
Db 108 QNEMDILVLGRIFPOYCSTAKKALKWYPLLGQFMAISGTTFLDRKDRTSVQTLGGAVK 167

Qy 237 -----QGVDMYLONG--SYRNTVASLETSEG---PIOPGSSLQKVMYLTPLSSN 283
Db 168 TIQSGNGKGQSVMFPECTRSYSKDVGIMPFKKGCFHLAVQSGAP-----IVPVVQN 221

Qy 284 KQR-----RGIALDGQI-----KRQD---OCLASTTLLAQPDQDRAFTGVILSY 318
Db 222 TSRMFSGRKGKDAGEILVDVLSPPIETKGLDASNVNDALMATTYKAMCETADQIG 275

RESULT 7
US-10-505-928-733
; Sequence 733, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.
 TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 FILE REFERENCE: 28967/39178
 CURRENT APPLICATION NUMBER: US/10/505,928
 CURRENT FILING DATE: 2004-08-27
 PRIORITY APPLICATION NUMBER: US 60/363,019
 PRIORITY FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 866
 SOFTWARE: PatentIn 3.2
 SEQ ID NO 733
 LENGTH: 893
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-505-928-733

Query Match 3.8%; Score 75.5; DB 6; Length 893;
 Best Local Similarity 19.7%; Pred. No. 5.1;
 Matches 95; Conservative 64; Mismatches 155; Indels 169; Gaps 22;
 QY 19 LYMGKRDVFV--HVSGVPEPDGIVVLDE--YIRDNRKVFGQIVCSFRYGRREEDEVNGLN 74
 Db 358 LIRGPLEYVPSAKVEEVRQAIPLDNEGIYVQDKVTGKVRavigstymltQDVL-- 414
 QY 75 FOKEELCLASEQIY----PRPEKSDEQTKLQERLLKKLGNSNAIPFTFNISPNSPSSVTL 129
 Db 415 WEKELPPGVEELNKQGDPLADRGEKOTAK-----SLQPLAPRNKTR 456
 QY 130 QGEGEDDNGDPGCGVSYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQ--G 179
 Db 457 V-----VSYRVPHNNAVQVYDREKRARVFGPELVSLGPEEQFTVLSLSAGR 505

QY 180 QQP-----CTLVRKDFMLSPELELEVTLDKOLYHLGERIGVNICIRNSNK---- 226
 Db 506 KRPHARRALCLLIGPDEFTD--VITIETADHARLQL---OLAYNNWHEVNDRKDPOETAK 560
 Qy 227 -----MVKKIKAMVQQGVWLF---QNGS--YRNTVASLETSEG---- 261
 Db 561 LFSVPDFVGACKAIASRVRGAVASVTFDDFHKN SARIIRTAVFGFETSEAKGPDGMLP 620
 Qy 262 -----CPIQP----GSSLQKVMYLTPLSSNQKRRGIALD--- 292
 Db 621 RPRDQAVFPONGLWSSVQSVEPVQDQRTRDALQRSVOLAIEITTNSQELAKHEAQLR 680
 Qy 293 -----GOIKRQ---DQCLA-----STTLAQPDQR----DAFGV 319
 Db 681 EOEARGRLERQKILDSEAEKARKELEALMSMAVESTGTAKAEAESRAEARIEEGGS 740
 Qy 320 ITISYAVKVKLFLGAGGELISAELPFV----LMHPKPGTKAKVITHADSDQADVET--FR 370
 Db 741 VL---OAKLKQALAIETEAELOQVQVRELELYVARAOLEEVSKAQQLAEVEVKFK 796

RESULT 8
 US-10-196-749-164
 Sequence 164, Application US/10196749
 Publication No. US20060094864A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Wattanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C340
 CURRENT APPLICATION NUMBER: US/10/196,749
 CURRENT FILING DATE: 2002-07-16
 PRIORITY APPLICATION NUMBER: 10/052586
 PRIORITY FILING DATE: 2002-01-15
 PRIORITY APPLICATION NUMBER: 60/059263
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/059266
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/062250
 PRIORITY FILING DATE: 1997-10-17
 PRIORITY APPLICATION NUMBER: 60/063120
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063486
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063540
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063541
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063544
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION data removed - See File Wrapper or PALM.
 SEQ ID NO 164
 LENGTH: 299
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-196-749-164

Query Match 3.8%; Score 74.5; DB 6; Length 299;
 Best Local Similarity 26.2%; Pred. No. 1;
 Matches 32; Conservative 21; Mismatches 44; Indels 25; Gaps 6;
 Qy 63 YGREEDEVNGLNFOKEELCLASEQIYVPRPEKS-----DKEQTKLQERLLKKLGSN-- 111
 Db 44 FGTTEEEI----QEICETLRLYTRKKPNYELKEVEKAQKLKAKGLNPDG 97
 Qy 112 --AIPFTFNISP-NAPSSVTLQQGHDNDGDPGCGVSYVKIFAGESETDRTHRRSTVTLGI 168
 Db 98 TPALSTLGGFSPASKPSSPREVKABEKS---PISINVKTVKKEPE-DRQASKSPYNGV 152
 Qy 169 RK 170
 Db 153 RK 154

RESULT 9
 US-11-170-482-16
 Sequence 16, Application US/11170482
 Publication No. US20060094037A1
 GENERAL INFORMATION:
 APPLICANT: St. George-Hyslop, Peter H.
 APPLICANT: Fraser, Paul E.
 APPLICANT: University of Toronto
 TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
 FILE REFERENCE: 1034/1H570
 CURRENT APPLICATION NUMBER: US/11/170,482
 PRIORITY APPLICATION NUMBER: US/09/945,258
 PRIORITY FILING DATE: 2001-08-31
 PRIORITY APPLICATION NUMBER: US 60/229,889
 PRIORITY FILING DATE: 2000-09-01
 PRIORITY FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 16
 LENGTH: 708
 TYPE: PRT
 ORGANISM: mouse
 US-11-170-482-16

Query Match 3.8%; Score 74.5; DB 7; Length 708;
 Best Local Similarity 19.3%; Pred. No. 4.4; Mismatches 102; Indels 101; Gaps 14;
 Matches 59; Conservative 44; Mismatches 102; Indels 101; Gaps 14;

Qy 6 KVFKKC-----APNGKVTLY-MGKRDVFVHSVGEPIGDIVLDEYIRDNRKVFGQIV 58
 Db 189 KVIKQCYODHNLGQNGSAPSFPPLCAMQLFSHMHAV--ISTATCMRSFIQSFSINPEIV 246

Qy 59 CSFRYGREEDEVMLNFOKECLASEQIYPRPE-KSDKEQTKLQERLKKIGSNAIPFTF 117
 Db 247 C-----DPLSDYNWWSMLKPINTSVGLEPDVRVVAAATRILDSR-----SFFW 288

Qy 118 NISPNAAPSSVTLLQQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIOFA-- 174
 Db 289 NVAPGAESAV-----ASFVTQLAEEA---LHKAPDVTLISRNVMFVFQ 330

Qy 175 -----PTKGQQOPCTLVRKDFMLSPGELELEVTLKQLYLHGBERIGNICI 220
 Db 331 GETFDYIGSSRMVYDMENGKFVRLLENIDSFVELGQVALRTSLD--LWMH----- 378

Qy 221 RNNNSNKKMKKKAMVQOGVVDVLFQNGSYRNTVASLETS-EGCP-----IQPGS 268
 Db 379 ---TDPMMSQKNESVKNQVEDL-----LATTEKSGAGVPEWVLRRLAQSOALPPS 424

Qy 269 SLQKVM 274
 Db 425 SLQRFL 430

RESULT 10

; Sequence 304, Application US/10505928
 ; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505, 928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363, 019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 304

; LENGTH: 763

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-251-465-22

Query Match 3.7%; Score 72.5; DB 7; Length 806;
 Best Local Similarity 18.3%; Pred. No. 9.2; Mismatches 81; Conservative 73; Mismatches 81; Indels 143; Gaps 22; Matches 81; Conservative 73; Mismatches 81; Indels 143; Gaps 22;

Qy 11 CAPNGKVTLYMGKRDVFVHSVGEPIGDIVV-----LDDEYIRDNRKVFGQIV 58
 Db 61 CPPPGGGP--MGPTVWVKDGTGLVPSERVJVGQRLQVNASHEDSGAYSCRQRLTQRL 118

Qy 59 CSFRY-----GREEDEVMLNFOKECLASEQIYPRPE-KSDKEQTKLQERL 105
 Db 119 CHFSVRVTIDAPSSGDEDGEDEAEGTVD-----TGAPYWTPERMDK-----KLL 164

Qy 106 KKLSNAIPFTNTISPNA-PFSSVTLLQQGEDDNGDPGCVSYVKIFAGESETDRTHRSTV 164
 Db 165 AVPAANTVRFRCPAAGNPTPSISWLNGRE-----FRGE-----HRIGGI 204

Qy 165 TLGIRKIOFA-----PTKGQQOPCTL-----VRKDFML-----SPGELELEVTL-D-K 205
 Db 205 KU-RHQQWSLVMESVVPDSRGNYTCVVENKFGSIROTYLTDVLERSPHRPILOAGLPAN 262

Qy 206 QLYLHGERIGWNICIRNNNSNKKAMVQOGVVDVLFQNGSYRNTVASLETSEGCGIQ 265
 Db 263 QTAVLGSDEVFHCKVYDAOPHIQWLKHVBNGSKV-----GPDGTP-- 304

Qy 266 PGSSLQKVMVLTPLL-----SSNKORRGIALDGQIKRQD---OCLASTIL----- 307
 Db 305 -----YVTVLUKTAGANTTDKELEVLSLH-NVTFEDAGEYTCLAGNSIGFSHSAWL 354

Qy 308 -----LAQPDDQR-DAFGVVISYAVKVKFLGALGGELSAELPPVLMHMPKGPTKAKVI 358
 Db 355 VVLPAEEBELVEADEAGSVAGILSYGVGFILVVA---AVTLCRLRSPPKKGLGSPTV 411

Qy 359 HADSQADVETFRQDPTIDQASV 380
 Db 412 HKISRFPLK--RQVSLESNASM 431

RESULT 12

; Sequence 48, Application US/10322836
 ; Publication No. US20060090212A1

; GENERAL INFORMATION:

; APPLICANT: Turner, Alexander C., Jr.

APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT FILING DATE: 2002-12-18
; PRIORITY FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 48
; LENGTH: 1075
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (130)..(130)
; OTHER INFORMATION: Xaa = Gln or STOP
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (179)..(179)
; OTHER INFORMATION: Xaa = Ser or Gly
; US-10-322-836-48

Query Match 3.7%; Score 72.5; DB 6; Length 1075;
Best Local Similarity 16.8%; Pred. No. 15;
Matches 48; Conservative 48; Mismatches 94; Indels 95; Gaps 11;

Qy 17 VTLVYMGKRFDFDVHVGVERPIDGIVLVLDEYIRD---NRKVFGQIVCSFRYGREEDEVNG 72
Db 101 LVLHQTRRRESRDHAT-----LNDIFMNINVRLSIXEDVIRLFKKSKKE---IG 146
Qy 73 LINFOKELCIASEQIYPP-----RPEKSDEQTKLQERLLKKLKGNSNAIPFTFNI 119
Db 147 LQMHHEELLKVTNELYTVMKTYHMYHAESISAEKLKEAKQEEKQFNKSGD----- 197
Qy 120 SPNAPSSVTLOQGEDDNGDPGCVSYVKIFAGESEETDRTHRSTVTLGIRKIQPAPTK-- 177
Db 198 -----LSMNLRLHE-----DRPQRSSV---KKIEKMEKERO 226
Qy 178 -----OGOQPCTLVRKDFMLSPGEBLEBLTDLKOLYLVHGERIGVNICRNNSNKNVKIKA 233
Db 227 AKYSENKLKCTKARNDDYLNLAATNAIS---KYYIHDVSIDLBCCDLGFEHASLARTERT 283
Qy 234 MV-----QQGVW---LFQONGSYRNTVASLETSEGCP 263
Db 284 YLSAEYNLETSRHEGLDVVIENAVDNLDSDRSRKHTVMDMCNQVFPC 328

RESULT 13

US-10-505-928-310 Application US/10505928
; Sequence 310, Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/325,899
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2451
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-310

Query Match 3.6%; Score 71; DB 6; Length 798;
Best Local Similarity 19.7%; Pred. No. 13;
Matches 43; Conservative 33; Mismatches 88; Indels 54; Gaps 8;

Qy 48 RDNRKVFGQIVCSFRYGREEDEWMLNFQKELCIASEQIYPRPEKSDEQTKLQERLUK- 106
Db 8 QDSESVWSDIECAALVGEDQ-----PLC-----PDPELDSELVDNLDLT 48

Qy 107 -----KLGSNAIPFTFNIISPNAPSSVTLOQGEDDNG-----DPCGVSY 144

Best Local Similarity 21.4%; Pred. No. 52;
Matches 86; Conservative 50; Mismatches 137; Indels 129; Gaps 22;

Qy 12 APNGKVTLVYMGKRFDFDVHVGVERPIDGIVLVLDEYIRD-NRKVFGQIVCSFRYGR---- 65
Db 963 APSGFEDLERGRREMVE-----EDLDAALPLPDEDEEDISEYKFAATYFOGTTTHSY 1017
Qy 66 -----EEDE-----VMGLNFQKELCLASEQIYPRPE---KSDKEQ--- 97
Db 1018 TRRPLKOPPLVHDDEGDQLAALAVWITLRFMGL-----PEPYKHTAMSDGEKIP 1069

Qy 98 --TKLQERLLKKLGSNAIPFTFNISPNAPESSVTLOQGEDDNGDPCG-----VS 143
Db 1070 VMTKIVYETLGKK-----TYK-----REIQLAQGEGEAQLPPEGOKKSSVRHKLVHLT 1115
Qy 144 YYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMFLSPGEL---- 197
Db 1116 LKKSKSLTEEVTKRLHDGESTVOQNSMLEDRPTS-----NLEKLHFIIGNGILRPALRD 1169
Qy 198 ELEVTLDKQL-----YLHGERIGVNICIR--NNSNMVKKIKAMVQQG-VDWLFQN 246
Db 1170 EYCOISKQLTHNPKSSYARG-WILVSLCVGCFAPESEKFVKYLRNFIHGPPGYAPCE 1228
Qy 247 GSYRNTVASLETSEGCP1QPGSSLQKVWLYTPLLSSNKRRTIAL----DGQIKRQDQC 301
Db 1229 ERLRRTFVN----GTRTOPPSWLE-----LQATSKKKPIMLPVTFMGTTKLLTD 1275

Qy 302 LAST-----TLLAQPDQDAFGVIIISYAVKVLF--LGALG 335
Db 1276 SATTAKELCNALADKISLKDRCFG---FSLYIALFDKVSSLG 1313

RESULT 14

US-10-511-937-2451
; Sequence 2451, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/325,899
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2451
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2451

us-10-056-405-2.rapbn

RESULT 15
US-11-316-132-1
• Sequence 1: Application US/11316132

GENERAL INFORMATION:
APPLICANT: Shridhar, Viji
APPLICANT: Roberts, Lewis R.
APPLICANT: Kaufmann, Scott H.
TITLE OF INVENTION: HSulf-1 Nucleic Acids, Polypeptides and
TITLE OF INVENTION: Methods of Using
FILE REFERENCE: 07039/449001
CURRENT APPLICATION NUMBER: US/11/316,132
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/778,607
PRIOR FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 60/446,945
PRIOR FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
US-11-316-132-1

Query	Match	Score	71;	DB	7;	Length	871;		
Best	Local	Similarity	28.6%	Pred.	No.	15;			
Matches	30;	Conservative	16;	Mismatches	35;	Indels	24;	Gaps	6
Qy	6 KVFKKC--APNGKV---TLXMGKRDVFVDHVS GVEPIDGV IWLDD EYIRDNRKVFGQIVC	59							
Db	613 RVT HKC FILPND S IHCERELYQSARAWDKHAKID--KEIA LQDK-IKNLRE YFGHL-	657							
Qy	60 SFRYGRE DEEV MGLNF Q KELCLASE QIYP PREPKSD KEQT KLQ ERL	104							
Db	668 --KRRKPEE-----CS CSKQSY YNNKE GVKKQEK L KSHL	699							

Search completed: May 20, 2006, 23:06:54
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:06:58 ; Search time 196 Seconds
 (without alignments)
 893.438 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 383
 Sequence: 1 MVNENFKVKKCAPNGKVLY.....ADVETFRQDTIDQQASVDFE 383
 Scoring table: Oligo Gapop 60.0 , Gapext 60.0
 Word size : 1
 Total number of hits satisfying chosen parameters: 2589203
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	383	100.0	383	5 ABP52833
2	383	100.0	383	7 ABR84476
3	20	5.2	364	4 ABB61736
4	20	5.2	364	8 ADQ89588
5	11	2.9	382	4 AAG67785
6	11	2.9	398	7 ABR84484
7	11	2.9	401	4 ABB61964
8	11	2.9	409	4 AAG67784
9	11	2.9	409	4 AAG67781
10	11	2.9	409	7 ADE58183
11	11	2.9	409	7 ADE58179
12	11	2.9	409	7 ADN95251
13	11	2.9	409	9 ADY15068
14	11	2.9	410	5 ABG69496
15	11	2.9	410	7 ADE58177
16	11	2.9	410	7 ADE58181
17	11	2.9	479	10 AEF35190
18	11	2.9	492	10 AEF35191
19	11	2.9	526	8 ADR23187
20	11	2.9	526	8 ADR23186
21	11	2.9	388	4 AAG67782
22	9	2.3	388	4 AAG67783

ALIGNMENTS

24	9	2.3	388	9 ADX07504	Adx07504 Cyclin-de
25	9	2.3	394	9 AED51702	Aed51702 Pig arres
26	9	2.3	470	4 ABB58174	Abb58174 Drosophil
27	8	2.1	22	7 ADJ94231	Adj94231 Self-anti
28	8	2.1	38	4 AAM20580	Aam20580 Peptide #
29	8	2.1	38	4 ABB41697	Abb41697 Peptide #
30	8	2.1	38	4 AAM35493	Aam35493 Peptide #
31	8	2.1	38	4 ABB25470	Abb25470 Protein #
32	8	2.1	38	4 AAM75381	Aam75381 Human bon
33	8	2.1	38	4 AAM62570	Aam62570 Human bra
34	8	2.1	38	4 ABG57138	Abg57138 Human liv
35	8	2.1	38	5 ABG44975	Abg44975 Human pep
36	8	2.1	180	6 ADA0634	Ada0634 Human bet
37	8	2.1	182	7 ADD27419	Add27419 Human adi
38	8	2.1	182	7 ADD27127	Add27127 Human adi
39	8	2.1	182	7 ADD27197	Add27197 Human adi
40	8	2.1	187	6 ABU70623	Abu70623 Human adi
41	8	2.1	187	7 ADD27507	Add27507 Human adi
42	8	2.1	204	2 AAW20559	Aaw20559 Helicobac
43	8	2.1	204	2 AAW24688	Aaw24688 H. pylori
44	8	2.1	212	4 AAG73899	Aag73899 Human col
45	8	2.1	279	7 ABO78668	Ab078668 Pseudomon

CC (see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its complement; and (2) a method for identifying an agent that binds to mosquito olfaction molecules comprising: (a) providing an isolated mosquito olfaction molecule; (b) contacting a test agent with the isolated mosquito olfaction molecule; and (c) detecting specific binding of the test agent to the isolated mosquito olfaction molecule, where the presence of specific binding identifies the test agent as a mosquito olfaction-binding compound. The mosquito olfaction molecules are useful for mosquito management, i.e. controlling this pest and disease vector. A method from the present invention of screening for substances that modulate arrestin-odorant receptor interaction is useful for identifying arrestin 1 from the present invention

CC pest control agents. The present sequence represents *Anopheles gambiae*

CC XX SQ Sequence 383 AA:

Query Match 100.0%; Score 383; DB 5; Length 383;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MVYNFKVKKKCACPNGKVLYMGRDFVDFHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60

Db 1 MVYNFKVKKKCACPNGKVLYMGRDFVDFHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60

QY 61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

Db 61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

QY 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

QY 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQQGD 240

Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQQGD 240

QY 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLISSNKQRGGIALDGOIKRQQ 300

Db 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLISSNKQRGGIALDGOIKRQQ 300

QY 301 CLASTILLAQPDDAFGVIIYAVKVLFLGALGGELSAELPFVLMHPKPGTAKVIHA 360

Db 301 CLASTILLAQPDDAFGVIIYAVKVLFLGALGGELSAELPFVLMHPKPGTAKVIHA 360

QY 361 DSQADVENTFRQDTIDQQASVDFE 383

Db 361 DSQADVENTFRQDTIDQQASVDFE 383

RESULT 2

ABR84476 ID ABR84476 standard; protein; 383 AA.

XX AC ABR84476;

XX DT 15-JAN-2004 (first entry)

XX DE Mosquito olfaction molecule, arrestin 1.

XX ARRESTIN 1; MOSQUITO; OLFACTION; INSECTICIDE; ANTIMALARIAL.

OS Anopheles gambiae.

XX WO2003076590-A2.

XX PD 18-SEP-2003.

XX PF 10-MAR-2003; 2003WO-US007174.

XX PR 08-MAR-2002; 2002US-00094240.

XX PA (UYVA-) UNIV VANDERBILT.

PI Zwiebel LJ;

XX WPI; 2003-722331/68.

DR N-PSDB; ACF79716.

XX PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.

XX PT

XX PS Claim 1; Fig 2; 101pp; English.

XX SQ Sequence 383 AA:

Query Match 100.0%; Score 383; DB 7; Length 383;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MVYNFKVKKKCACPNGKVLYMGRDFVDFHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60

Db 1 MVYNFKVKKKCACPNGKVLYMGRDFVDFHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60

QY 61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

Db 61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

QY 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 121 PNAPSSVTLOQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

QY 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQQGD 240

Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQQGD 240

QY 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLISSNKQRGGIALDGOIKRQQ 300

Db 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLISSNKQRGGIALDGOIKRQQ 300

QY 301 CLASTILLAQPDDAFGVIIYAVKVLFLGALGGELSAELPFVLMHPKPGTAKVIHA 360

Db 301 CLASTILLAQPDDAFGVIIYAVKVLFLGALGGELSAELPFVLMHPKPGTAKVIHA 360

QY 361 DSQADVENTFRQDTIDQQASVDFE 383

Db 361 DSQADVENTFRQDTIDQQASVDFE 383

RESULT 3

ABB61736 ID ABB61736 standard; protein; 364 AA.

XX AC ABB61736;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 12000.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX DR
 XX DR N-PSDB; ADQ89587.
 XX PT New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell
 PT proliferative diseases (e.g. cancer) or for identifying modulators of
 PT mitosis or meiosis.
 XX PT
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PA
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL05839.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 12000; 21pp + Sequence Listing; English.
 XX CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
 ABL2072). The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 364 AA;
 Query Match 5.2%; Score 20; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 228 VKKIKAMVQQGVDFVLFQNG 247
 Db 227 VKKIKAMVQQGVDFVLFQNG 246
 XX RESULT 4
 ADQ89588 ADQ89588 standard; protein; 364 AA.
 AC ADQ89588;
 XX
 XX DE An exemplary phosphorylation-independent arrestin mutant.
 XX KW Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalciuric hypercalcemia; hyperparathyroidism;
 KW neurological disorder.
 XX OS Unidentified.
 XX PN WO200167106-A2.
 XX PD 13-SEP-2001.
 XX PF 05-MAR-2001; 2001WO-US007304.
 XX PR 03-MAR-2000; 2000US-0186706P.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PT Bernstein G;
 XX DR
 XX WPI; 2001-602637/68.
 XX PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.
 XX PS Disclosure; Page 47; 47pp; English.

XX
 CC The present sequence represents an exemplary phosphorylation-independent
 CC arrestin mutant. Such mutants are used in screening assays to identify
 CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A
 CC method for identifying a GPCR ligand comprises contacting a composition
 CC comprising the GPCR and a constitutively active arrestin mutant with a
 CC test compound; and determining the ability of the test compound to
 CC modulate binding of arrestin mutant to the GPCR, where modulation of
 CC binding indicates that the test compound is a GPCR ligand. The method is
 CC used for identifying potential ligands and/or modulators of GPCRs,
 CC particularly modulators, for use as human therapeutics. Modulators of
 CC GPCR may be used for treating patients having e.g. retinitis pigmentosa,
 CC stationary night blindness, colour blindness, nephrogenic DI, isolated
 CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial
 CC hypocalciuric hypercalcemia, hyperparathyroidism and neurological
 CC disorders. The methods may be used for screening pluralities of test
 CC compounds (e.g. a small molecule library of compounds) or a composition
 CC containing a plurality of GPCRs. The methods may be used in screening
 CC assays for identification of natural and surrogate agonists of orphan
 CC GPCRs, and for identification of GPCR antagonists and/or agonists
 XX
 SQ Sequence 382 AA;

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

RESULT 6

Query Match		Score 11; DB 4; Length 382;	
Best Local Similarity		Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;	
QY	341	ELPFFVLMHPKP	351
Db	339	ELPFFVLMHPKP	349

Query Match 2.9%; Score 11; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy |||||||
 62 RYGREEDEVMG 72
 Db 61 RYGREEDEVMG 71

RESULT 8
 AAG67784
 ID AAG67784 standard; protein; 409 AA.
 XX
 AC
 XX
 AAG67784;
 DT 10-DEC-2001 (first entry)
 XX
 DE An exemplary phosphorylation-independent arrestin mutant.
 XX
 DE Arrestin; phosphorylation-independent arrestin mutant.
 KW Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalciuric hypercalcemia; hyperparathyroidism;
 KW neurological disorder.

XX
 OS Unidentified.
 XX
 PN WO200167106-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007304.
 XX
 PR 03-MAR-2000; 2000US-0186706P.
 XX
 PA (MILL-) MILLENNUM PHARM INC.
 PI Bernstein G;
 XX
 DR WPI; 2001-602637/68.
 XX
 PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.
 XX
 PS Disclosure; Page 47; 47pp; English.

XX
 CC The present sequence represents an exemplary phosphorylation-independent arrestin mutant. Such mutants are used in screening assays to identify PT retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX
 DR WPI; 2001-602637/68.
 XX
 PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX
 PS Disclosure; Page 46; 47pp; English.

XX
 CC The present sequence represents an arrestin protein. The specification describes phosphorylation-independent arrestin mutants. These mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR comprising contacting a composition comprising a GPCR and a constitutively active arrestin mutant with a test compound, and determining the ability of the test compound to modulate binding of the test compound; and determining the ability of the test compound to modulate binding of a modulator of arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a plurality of GPCRs). The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists

XX
 Sequence 409 AA;

Query Match 2.9%; Score 11; DB 4; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy |||||||
 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 9
 AAC67781
 ID AAC67781 standard; protein; 409 AA.
 XX
 AC AAC67781;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Amino acid sequence of human beta-arrestin 2.
 XX
 DE Arrestin; phosphorylation-independent arrestin mutant.
 KW Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism; neurological disorder.

XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 156..185
 FT /note= "putative phosphorylation-recognition region"
 XX
 PN WO200167106-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007304.
 XX
 PR 03-MAR-2000; 2000US-0186706P.
 XX
 PA (MILL-) MILLENNUM PHARM INC.
 XX
 PI Bernstein G;
 XX
 DR WPI; 2001-602637/68.
 XX
 PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX
 PS Disclosure; Page 46; 47pp; English.

XX
 CC The present sequence represents an arrestin protein. The specification describes phosphorylation-independent arrestin mutants. These mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR comprising contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a test compound, and determining the ability of the test compound to modulate binding of the test compound to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a plurality of GPCRs). The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists

XX
 Sequence 409 AA;

Query Match 2.9%; Score 11; DB 4; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy |||||||
 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 9
 AAC67781
 ID AAC67781 standard; protein; 409 AA.
 XX
 AC AAC67781;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Amino acid sequence of human beta-arrestin 2.
 XX
 DE Arrestin; phosphorylation-independent arrestin mutant.
 KW Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism; neurological disorder.

XX
 OS Homo sapiens.

Key	Location/Qualifiers
FT Region	156..185
FT /note= "putative phosphorylation-recognition region"	

XX
 PN WO200167106-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007304.
 XX
 PR 03-MAR-2000; 2000US-0186706P.
 XX
 PA (MILL-) MILLENNUM PHARM INC.
 XX
 PI Bernstein G;
 XX
 DR WPI; 2001-602637/68.
 XX
 PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX
 PS Disclosure; Page 46; 47pp; English.

XX
 CC The present sequence represents an arrestin protein. The specification describes phosphorylation-independent arrestin mutants. These mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR comprising contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a test compound, and determining the ability of the test compound to modulate binding of the test compound to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a plurality of GPCRs). The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists

XX
 Sequence 409 AA;

Query Match 2.9%; Score 11; DB 4; Length 409;
Best Local Similarity 100.0%; Pre. No. 0.13; Min. ID 1

specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC <http://www.wipo.int/pctdb/patent/sequence.html>
XX

of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by this inventor using the source data given in table 14 of the specification.

	Query	Match	Score	DB	Length				
Qy	ELPFVLMHPKP	2.9%	11	7	409				
Db	ELPFVLMHPKP	100.0%	Pred. No.	0.13					
		Matches	11; Conservative	0;	Mismatches	0;	Indels	0;	Gaps
	341	351							
	339	349							

Sequence 409 AA;
Query Match 2.9%; **Score** 11; **DB** 7; **Length** 409;
Best Local Similarity 100.0%; **Pred. No.** 0.13;
Matches 11; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;
DY 341 ELPFVLMPKRP 351
DP 339 ETPFVLMHPKP 349

Oy	341	ELPFVLMHPKP	351		Oy	341	ELPFVLMHPKP	351	
Db	339	ELPFVLMHPKP	349		Db	340	ELPFVLMHPKP	350	
RESULT 14					RESULT 15				
ABG69496			ID ADE58177		ABG69496			ID ADE58177	
ID ABG69496 standard; protein; 410 AA.	XX		XX ADE58177;		Rat bait protein beta arrestin 2.	XX		XX ADE58177;	
AC	XX		AC		DE Rat bait protein beta arrestin 2.	XX		AC	
XX			XX		DE Rat bait protein beta arrestin 2.	XX		XX	
DT 21-OCT-2002 (first entry)			XX		DE Rat bait protein beta arrestin 2.	XX		XX	
XX			XX		DE Rat bait protein beta arrestin 2.	XX		XX	
DE Rat bait protein beta arrestin 2.			XX		DE Rat bait protein beta arrestin 2.	XX		XX	
KW Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.	XX		XX		KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.	XX		XX	
XX Rattus sp.	OS		XX		Rattus norvegicus.	OS		OS	
OS Rattus sp.	XX		XX		Rattus norvegicus.	OS		OS	
PN WO200253726-A2.			XX		PN WO200316475-A2.	XX		XX	
XX			XX		XX			XX	
PD 11-JUL-2002.			XX		PD 27-FEB-2003.	XX		PD 27-FEB-2003.	
XX			XX		XX			XX	
PF 28-DEC-2001; 2001WO-EP015423.			XX		PF 14-AUG-2002; 2002WO-US025765.	XX		PF 14-AUG-2002; 2002WO-US025765.	
XX			XX		XX			XX	
PR 02-JAN-2001; 2001US-0259377P.			XX		PR 14-AUG-2001; 2001US-0312147P.	XX		PR 14-AUG-2001; 2001US-0312147P.	
XX			XX		PR 01-NOV-2001; 2001US-0346382P.	XX		PR 01-NOV-2001; 2001US-0346382P.	
PA (HYBR-) HYBRIGENICS.			XX		PR 26-NOV-2001; 2001US-0333347P.	XX		PR 26-NOV-2001; 2001US-0333347P.	
PA (CNRS) CENT NAT RECH SCI.			XX		PA (GEHO) GEN HOSPITAL CORP.	XX		PA (GEHO) GEN HOSPITAL CORP.	
PA (FARB) BAYER AG.			XX		PA (FARB) BAYER AG.	XX		PA (FARB) BAYER AG.	
PT Legrain P, Marullo S, Jockers R;			XX		PT Woolf C, D'urso D, Befort K, Costigan M;	XX		PT Woolf C, D'urso D, Befort K, Costigan M;	
PT DR N-PSDB; ABSS51032.			XX		PT DR N-PSDB; ABSS51032.	XX		PT DR N-PSDB; ABSS51032.	
XX Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.			XX		XX WPI; 2003-268312/26.	XX		XX WPI; 2003-268312/26.	
PT WPI; 2002-583612/62.			XX		XX GENBANK; P29067.	XX		XX GENBANK; P29067.	
PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.			XX		PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	XX		PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	
PS Claim 1; Page 53; 125pp; English.			XX		PS Claim 1; Page; 1017pp; English.	XX		PS Claim 1; Page; 1017pp; English.	
XX The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two- hybrid assay			XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.			XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.			
SQ Sequence 410 AA;			XX Sequence 410 AA;		SQ Sequence 410 AA;			SQ Sequence 410 AA;	
Query Match 2.9%; Score 11; DB 5; Length 410;			Best Local Similarity 100.0%; Pred. No. 0.13;		Query Match 2.9%; Score 11; DB 5; Length 410;			Best Local Similarity 100.0%; Pred. No. 0.13;	
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Query Match 2.9%; Score 11; DB 7; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 341 ELPFVLMHPKP 351
| | | | | | | | | |
Db 340 ELPFVLMHPKP 350

Search completed: May 20, 2006, 23:10:23
Job time : 198 sec

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A;Residues: 1-363 <PLA>
 A;Cross-references: UNIPROT:P51486; UNIPARC:UPI000126075; GB:X79072; NID:9483527; PIDN:
 A;Note: the source is designated as Calliphora erythrocephala
 C;Superfamily: arrestin

Query Match 4.4%; Score 17; DB 2; Length 363;
 Best Local Similarity 100.0%; Pred. No. 4e-09; Mismatches 17; Conservative 0; Indels 0; Gaps 0;
 Matches 17;

Qy 322 SYAVKVKLFLGALGGEL 338
 Db 321 SYAVKVKLFLGALGGEL 337

RESULT 3
 B56607
 arrestin homolog - tobacco budworm
 C;Species: Heliothis virescens (tobacco budworm)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C;Accession: B56607
 R;Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
 Cell. Signal. 5, 69-80, 1993
 A;Title: Arrestin-subtypes in insect antennae.
 A;Reference number: A56607; MUID:9319955; PMID:8452755
 A;Accession: B56607
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-381 <RAM>
 A;Cross-references: UNIPROT:P55274; UNIPARC:UPI000126089
 A;Experimental source: antennae
 A;Note: sequence extracted from NCBI backbone (NCBIP:127926)
 C;Superfamily: arrestin

Query Match 4.2%; Score 16; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 4.5e-08; Mismatches 16; Conservative 0; Indels 0; Gaps 0;
 Matches 16;

Qy 1 MVYNFKVFKKCAPNGK 16
 Db 1 MVYNFKVFKKCAPNGK 16

RESULT 4
 A56607
 arrestin homolog - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C;Accession: A56607
 R;Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
 Cell. Signal. 5, 69-80, 1993
 A;Title: Arrestin-subtypes in insect antennae.
 A;Reference number: A56607; MUID:9319955; PMID:8452755
 A;Contents: antennae
 A;Accession: A56607
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-407 <RAM>
 A;Cross-references: UNIPROT:P32122; UNIPARC:UPI000126088; GB:S57174; NID:9298755; PIDN:
 A;Note: sequence extracted from NCBI backbone (NCBIN:127923, NCBIP:127925)
 C;Superfamily: arrestin

Query Match 3.1%; Score 12; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 0.00064; Mismatches 12; Conservative 0; Indels 0; Gaps 0;
 Matches 12;

Qy 62 RYGRBEEDEVMG 73
 Db 69 RYGRBEEDEVMG 80

RESULT 5
 A34856
 49K photoreceptor protein - fruit fly (Drosophila melanogaster)

RESULT 6
 S11566
 arrestin homolog - fruit fly (Drosophila miranda)
 C;Species: Drosophila miranda
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S11566
 R;Krishnan, R.; Ganguly, R.
 Nucleic Acids Res. 18, 5894, 1990
 A;Title: Nucleotide sequence of the arrestin-like 49 Kd protein gene of Drosophila miranda
 A;Reference number: S11566; MUID:91016944; PMID:2216789
 A;Accession: S11566
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-401 <KRI>
 A;Cross-references: UNIPROT:P19108; UNIPARC:UPI000126082; EMBL:X54084; NID:97612; PIDN:
 C;Genetics:
 A;Gene: FlyBase:Dmir/Arr2
 A;Cross-references: FlyBase:FBgn0012552
 A;Introns: 286/1; 351/1
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.0068; Mismatches 11; Conservative 0; Indels 0; Gaps 0;
 Matches 11;

Qy 62 RYGRBEEDEVMG 72
 Db 61 RYGRBEEDEVMG 71

RESULT 7
 B55081
 arrestin 2 - bluebottle fly (Calliphora vicina)
 C;Species: Calliphora vicina
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C;Accession: B55081; S44292
 R;Planger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
 J. Biol. Chem. 269, 26969-26975, 1994
 A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
 A;Reference number: A55081; MUID:95014564; PMID:7929436
 A;Accession: B55081
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-401 <PLA>
 A;Cross-references: UNIPROT:P51487; UNIPARC:UPI00016B8DC; EMBL:X79073; NID:9483583; PID:
 A;Note: the source is designated as Calliphora erythrocephala
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 RYGRREDEVNG 72
 Db 61 RYGRREDEVNG 71

RESULT 8

S68254 arrestin isoform 2S, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 CAccession: S68254
 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Accession: S68254
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-405 <JAH>
 A;Cross-references: UNIPROT:P51467; UNIPARC:UPI000012607C; GB:U48410
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 9

S68253 arrestin isoform 1S, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 CAccession: S68253
 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Accession: S68253
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-407 <JAH>
 A;Cross-references: UNIPROT:P51466; UNIPARC:UPI0000126077; GB:U48410; NID:g1215723; PIDN
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 10

S18984 arrestin - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 CAccession: S18984
 R;Rapoport, B.; submitted to the EMBL Data Library, November 1991
 A;Description: Isolation of a novel cDNA belonging to the arrestin family from human thy
 A;Reference number: S18984
 A;Accession: S18984

RESULT 11

A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-409 <RAP>
 A;Cross-references: UNIPROT:P32121; UNIPARC:UPI000016A58B; EMBL:Z11501; NID:g28850; PIDN
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 12

S68255 arrestin isoform 1L, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 CAccession: S68255
 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Accession: S68255
 A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA
 A;Residues: 1-415 <JAH>
 A;Cross-references: UNIPROT:P51463; UNIPARC:UPI000012607E; GB:U48410
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.007; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 347 ELPFVLMHPKP 357

RESULT 13

arrestin arr3L - bovine

N;Contains: arrestin arr3S

C;Species: Bos primigenius taurus (cattle)

C;Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: A47140; B47140; JC2051

R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donobo, L.A.
J. Biol. Chem. 268, 15640-15648, 1993

A;Title: Polypeptide variants of beta-arrestin and arrestin3.

A;Reference number: A47140; MUID:93340166; PMID:8340388

A;Accession: A47140

A;Molecule type: mRNA

A;Residues: 1-420 <STE>

A;Cross-references: UNIPROT:P32120; UNIPARC:UPI0000178BC2; GB:L14641

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBTP:136007)

A;Accession: B47140

A;Molecule type: mRNA

A;Residues: 1-362,374-420 <ST2>

A;Cross-references: UNIPARC:UPI0000178BC3

C;Comment: This protein plays a role in the regulation of G-protein-coupled receptors.

C;Superfamily: arrestin arr3L #status predicted <MAT>
 F;1-420/Product: arrestin arr3L #status predicted <MA2>
 F;1-362,374-420/Product: arrestin arr3S #status predicted <MA2>

Query Match 2.9%; Score 11; DB 2; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.0071; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 14

155423

arrestin-C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 13-Sep-1998

C;Accession: I55423

R;Craft, C.M.; Whitmore, D.H.; Weichmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994

A;Title: Cone arrestin identified by targeting expression of a functional family.

A;Reference number: 155423; MUID:94140898; PMID:8308033

A;Accession: I55423

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-387 <RES>

A;Cross-references: UNIPARC:UPI0000178BC4; EMBL:U03626; NID:g458200; PID:g458201

C;Superfamily: arrestin

Query Match 2.3%; Score 9; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 0.77; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDVFVDHV 30
 Db 19 GKRDVFVDHV 27

RESULT 15

S38943

arrestin - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C;Accession: S38943

R;Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, G.
FEBS Lett. 334, 203-209, 1993

A;Title: X-arrestin: a new retinal arrestin mapping to the X chromosome.

A;Reference number: S38943; MUID:94039835; PMID:8224247

A;Accession: S38943

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-388 <MR>

A;Cross-references: UNIPROT:P36575; UNIPARC:UPI000004230C; GB:S66793; NID:g439830; PID:NID:g439830

C;Superfamily: arrestin

Query Match 2.3%; Score 9; DB 2; Length 388;
 Best Local Similarity 100.0%; Pred. No. 0.77; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDVFVDHV 30
 Db 19 GKRDVFVDHV 27

Search completed: May 20, 2006, 23:16:16
 Job time : 42 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:07:08 ; Search time 301 Seconds
 (without alignments)
 1177.013 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 383
 Sequence: 1 MVYNFKVKKKCAPNGKVTLY.....ADVETFRQDTIDQOASVDFF 383

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	383	100.0	383	2	Q7PMG5_ANOGA	Q7pmg5 anopheles g
2	383	100.0	383	2	Q95NF3_ANOGA	Q95nf3 anopheles g
3	245	64.0	245	2	Q6VPP0_ANOGA	Q6vpp0 anopheles g
4	233	60.8	269	2	Q5TNW2_ANOGA	Q5tnw2 anopheles g
5	25	6.5	381	2	Q9BIG9_9NEOP	Q9big9 ascalaphus
6	20	5.2	364	1	ARRH_DROME	P15372 drosophila
7	18	4.7	18	2	Q7YT9V_ANOST	Q7ytv9 anopheles s
8	18	4.7	18	2	Q7YTWO_9DIPT	Q7ytw1 anopheles p
9	18	4.7	18	2	Q7YTWT1_ANOAR	Q7ytwt1 anopheles a
10	17	4.4	363	1	ARRI_CALVI	P51486 caliphora
11	16	4.2	381	1	ARRH_HELV1	P55274 heliothis v
12	14	3.7	52	2	Q6X126_DROYA	Q6xi26 drosophila
13	13	3.4	400	1	ARRH_LIMPO	P51484 limulus pol
14	12	3.1	407	1	ARRH_LOCOMI	P32122 locusta mig
15	11	2.9	217	2	Q6BDZ5_HUMAN	Q6bdz5 homo sapien
16	11	2.9	390	2	Q5BIJ0_DROME	Q5bij0 drosophila
17	11	2.9	398	2	Q705Q8_ANOGA	Q7q5q8 anopheles g
18	11	2.9	400	1	ARRB_CALVI	P51487 calliphora
19	11	2.9	401	1	ARRB_DROME	P19107 drosophila
20	11	2.9	401	1	ARRB_DROMI	P19108 drosophila
21	11	2.9	402	2	Q3TRC8_MOUSE	Q3trc8 mus musculu
22	11	2.9	405	1	ARR2_ONCME	P51467 oncorthynchu
23	11	2.9	406	2	Q5F2D9_MOUSE	Q5f2d9 mus musculu
24	11	2.9	406	2	Q6PFK2_BRARE	Q6pfk2 brachydanio
25	11	2.9	407	1	ARR1_ONCME	P51466 oncorthynchu
26	11	2.9	408	2	Q6DFC4_XENLA	Q6dfc4 xenopus lae
27	11	2.9	408	2	Q6GPY2_XENLA	Q6gpy2 xenopus lae
28	11	2.9	408	2	Q7T2D2_BRARE	Q7t2d2 brachydanio
29	11	2.9	409	1	ARRB2_HUMAN	P32121 homo sapien
30	11	2.9	409	2	Q2PP19_HUMAN	Q2pp19 homo sapien
31	11	2.9	409	2	Q6ICT3_HUMAN	Q6ict3 homo sapien

ALIGNMENTS

RESULT 1
 Q7PMG5_ANOGA,
 ID Q7PMG5_ANOGA PRELIMINARY, PRT: 383 AA.
 AC Q7PMG5;
 DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
 DT 07-DEC-2004, sequence version 2.
 DT 07-FEB-2006, entry version 12.
 DE ENSANGP0000012569.
 GN ORFNAMES=ENSANGG0000010080;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 RN NCBI_TAXID=180454;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=PEST;
 RC The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 --!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 distributed under the Creative Commons Attribution-NoDerivs License
 prelimary data.

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CC DR GO; GO:0007600; P:sensory perception; IEA.
 CC DR GO; GO:0007165; P:signal transduction; IEA.

CC DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.

DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.

DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; Arrestin; 1.
 DR SEQUENCE; 383 AA; 42809 MW; FA946438592BB53E CRC64;

QY 1 MVYNFKVKKKCAPNGKVTLYNGKRDFFDVHVGVEPIDGIWVLDDDEYIRDNRKVFGQIVCS 60
 1 MVYNFKVKKKCAPNGKVTLYNGKRDFFDVHVGVEPIDGIWVLDDDEYIRDNRKVFGQIVCS 60

Db Q2pp19 homo sapien

DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS0295; ARRESTINS; 1.
 SQ SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;

Query Match 100.0%; Score 383; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 Db 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 120

Qy 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD 240
 Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD 180

Qy 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMWLPLISSNKRQGIALDGQIKRQDQ 300
 Db 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMWLPLISSNKRQGIALDGQIKRQDQ 300

Qy 301 CLASTTLLAQPDQDRAFTGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVHA 360
 Db 301 CLASTTLLAQPDQDRAFTGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVHA 360

Qy 361 DSQADVETFRQDTIDQQASVDFE 383
 Db 361 DSQADVETFRQDTIDQQASVDFE 383

RESULT 2
 ID Q95NF3_ANOGA PRELIMINARY; PRT; 383 AA.
 AC Q95NF3;
 DT 01-DEC-2001, integrated into UniProtKB/TREMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Arrestin.
 GN Name=Arri;
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=7165;

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Antennae, and Head;
 RX MEDLINE=21680430; PubMed=11822731; DOI=10.1073/pnas.022505499;
 RA Ricci I., Santolamazza F., Costantini C., Favia G.;
 RT "Molecular characterization and chromosomal mapping of transcripts having tissue-specific expression in the malaria mosquito anopheles gambiae: possible involvement in visual or olfactory processes.";
 RT Parasitol. Res. 88:1-8(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G3;
 RA Merrill C.E., Riesgo-Escobar J., Pitts R.J., Kafatos F.C.,
 RT "Visual arrestins in olfactory pathways of Drosophila and the malaria vector mosquito Anopheles gambiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638 (2002).

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CC EMBL; AJ304409; CAC39103.2; -; mRNA.
 DR EMBL; AY017417; AAG54081.1; -; mRNA.
 DR HSSP; P17870; 1G4M.

DR Ensembl; ENSANGG0000010080; Anopheles gambiae.
 DR GO; GO:000760; P:sensory perception; IEA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 PFam; PF02752; Arrestin_C; 1.
 PFam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS0295; ARRESTINS; 1.
 SQ SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;

Query Match 100.0%; Score 383; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVUNFKVFKKCAGNGKVTLQMGKRDQFDVHSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60
 Db 1 MVUNFKVFKKCAGNGKVTLQMGKRDQFDVHSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60

Qy 61 FRYGREEDEVMLNFOKECLASSEQIYPRPEKSDEQTKLQERLLKKLGSSNAIPFTFNIS 120
 Db 61 FRYGREEDEVMLNFOKECLASSEQIYPRPEKSDEQTKLQERLLKKLGSSNAIPFTFNIS 120

Qy 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 Db 121 PNAPSSVTLQQGEDDNGDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Qy 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD 240
 Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD 240

Qy 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMWLPLISSNKRQGIALDGQIKRQDQ 300
 Db 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMWLPLISSNKRQGIALDGQIKRQDQ 300

Qy 301 CLASTTLLAQPDQDRAFTGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVHA 360
 Db 301 CLASTTLLAQPDQDRAFTGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTAKVHA 360

Qy 361 DSQADVETFRQDTIDQQASVDFE 383
 Db 361 DSQADVETFRQDTIDQQASVDFE 383

RESULT 3
 ID Q6VPPO_ANOGA PRELIMINARY; PRT; 245 AA.
 AC Q6VPPO;
 DT 05-JUL-2004, integrated into UniProtKB/TREMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE Arrestin (Fragment).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=7165;

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=4ARR, Yaounde, and L3-5;
 RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AY333991; AAR01116.1; -; Genomic_DNA.
 DR EMBL; AY333992; AAR01117.1; -; Genomic_DNA.
 DR EMBL; AY333993; AAR01118.1; -; Genomic_DNA.
 DR EMBL; AY333995; AAR01120.1; -; Genomic_DNA.
 DR EMBL; AY333990; AAR01115.1; -; Genomic_DNA.
 DR EMBL; AY333996; AAR01121.1; -; Genomic_DNA.
 DR EMBL; AY333994; AAR01119.1; -; Genomic_DNA.
 DR HSSP; P08168; LAYR.
 DR GO; GO:000760; P:sensory perception; IEA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.

DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 FT NON_TER 1 1
 FT 245 245
 SQ SEQUENCE 245 AA; 27038 MW; 86D8FF4520115DASF CRC64;

Query Match 64.0%; Score 245; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.6e-236; Mismatches 0; Indels 0; Gaps 0;

QY 129 LQOGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOCCQPCFLVRK 188
 1 LQOGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOCCQPCFLVRK 60

QY 189 DFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDVLFQNGS 248
 61 DFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDVLFQNGS 120

QY 249 YRNTVASLETSEGCPPIOPGSSLOKVMYTPLLSNKQRGTAIDGQIKRQDQCLASTLL 308
 121 YRNTVASLETSEGCPPIOPGSSLOKVMYTPLLSNKQRGIAIDGQIKRQDQCLASTLL 180

QY 309 AQPDDQDAFGVITISYAVKVLFGLALGELSAELPFLVLMHPKGTKAKVTHADSDQAVET 368
 181 AQPDDQDAFGVITISYAVKVLFGLALGELSAELPFLVLMHPKGTKAKVTHADSDQAVET 240

QY 369 FRODT 373
 Db 241 FRODT 245

RESULT 4
 Q5TNW2_ANOGA PRELIMINARY; PRT; 269 AA.

ID Q5TNW2_ANOGA PRELIMINARY; PRT; 269 AA.

AC Q5TNW2; 07-DEC-2004, integrated into UniProtKB/TREMBL.

DT 07-FEB-2006, entry version 7.

DE ENSANGP0000027511 (Fragment).

GN ORFNames=ENSANGG0000010080;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;

OC Anophelinae; Anopheles.

OX [1] NCBI_TaxID=180454;

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;

RT "Anopheles gambiae re-annotation.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

RN EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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CC EMBL; AJ303080; CAC36938.1; -; mRNA.

CC HSSP; P17870; 1G4M.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR PANTHER; PTHR11792; Arrestin; 1.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR PROSITE; PR00309; ARRESTIN.

DR PROSITE; PS00295; ARRESTIN; 1.

DR SEQUENCE 381 AA; 42789 MW; 451DEF465969857D CRC64;

Query Match 6.5%; Score 25; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1e-15; Mismatches 0; Indels 0; Gaps 0;

QY 51 RKYFGQIVCSFRYGREREDEVWGLNF 75
 52 RKVFGQIVCSFRYGREREDEVWGLNF 76

DR PRINTS; PR00309; ARRESTIN.

- RESULT 6
- ARRA_DROME STANDARD PRT; 364 AA.
- ID P15372; Q9VJJA8; AC; DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
- DT 01-APR-1990, sequence version 1.
- DT 07-FEB-2006, entry version 58.
- DE Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).
- GN Name=Arr1; Synonyms=Arra; ORFNames=CG5711;
- OS Drosophila melanogaster (Fruit fly).
- OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
- NCBI_TaxID=7227;
- RN [1] NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
- MEDLINE=90138925; PubMed=1689056;
- Smith D.P., Sheih B.-H., Zuker C.S.; "Isolation and structure of an arrestin gene from *Drosophila*."; Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).
- RN [2] NUCLEOTIDE SEQUENCE.
- RX MEDLINE=90138926; PubMed=2105491;
- Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S., Benzer S.; RT "Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";
- RT Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).
- RN [3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
- RC STRAIN=Berkeley; RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
- RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasper K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of *Drosophila melanogaster*."; Science 287:2185-2195(2000).
- RN [4] GENOME REANNOTATION.
- RP
-
- RX MEDLINE=22426069; PubMed=12537572;
- RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., RA Lewis S.E.; "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review." Genome Biol. 3:RESEARCH0083 .1-RESEARCH0083 .22 (2002).
- RN [5]
- RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
- RC STRAIN=Berkeley; TISSUE=Head; RX MEDLINE=22426066; PubMed=12537569;
- RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Park S., Wan K.H., George R.A., Guarin H., Krommiller B., Paclob J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; "A *Drosophila* full-length cDNA resource." Genome Biol. 3:RESEARCH0080 .1-RESEARCH0080 .8 (2002).
- RN [6]
- RP PHOSPHORYLATION.
- RX MEDLINE=91282780; PubMed=1905538;
- RA Matsumoto H., Yamada T.; RT "Phosrestin I and II: arrestin homologs which undergo differential light-induced phosphorylation in the *Drosophila* photoreceptor in vivo." Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
- RN [7]
- RP FUNCTION.
- RX MEDLINE=93303590; PubMed=8316831;
- RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M., Zuker C.S.; "Arrestin function in inactivation of G protein-coupled receptor rhodopsin in vivo." Science 260:1910-1916(1993).
- CC -1- FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2 proteins are mediators of rhodopsin inactivation and are essential for the termination of the phototransduction cascade.
- CC -1- INTERACTION:
- CC Q9VIM6:CG10949; NbExp=1; IntAct=EBI-145156, EBI-153699; CC Q9VAR2:CG11881; NbExp=1; IntAct=EBI-145156, EBI-186540; CC Q9W3Q2:CG12155; NbExp=1; IntAct=EBI-145156, EBI-151455; CC Q9T1S6:CG3754; NbExp=1; IntAct=EBI-145156, EBI-190361; CC Q9VEP0:CG3995; NbExp=1; IntAct=EBI-145156, EBI-160250; CC Q9VTH5:CG6175; NbExp=1; IntAct=EBI-145156, EBI-86076; CC Q9VH18:CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350; CC -1- TISSUE SPECIFICITY: Expressed specifically and abundantly in the photoreceptors. Inner and outer segments, and the inner plexiform regions of the retina.
- CC -1- PTM: Phosphorylated, but does not undergo light-induced phosphorylation.
- CC -1- SIMILARITY: Belongs to the arrestin family.
- CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms> Distributed under the Creative Commons Attribution-NoDerivs License
- CC -----
- DR EMBL; M30177; -; NOT_ANNOTATED_CDS; Genomic_DNA.
- DR EMBL; M30140; AAA28380_1; -; Genomic_DNA.
- DR EMBL; AE003657; AAF53644_1; -; Genomic_DNA.
- DR EMBL; AY061824; AAL27635_1; -; mRNA.
- DR PIR; A34867; A34867.
- DR HSSP; P17870; 1G4M.
- DR Intact; P15372; -; Ensembl; CG5711; Drosophila melanogaster.
- DR FlyBase; FBgn000120; Arr1.
- DR BiOCYC; DMEL-XXX-02:DMEL-XXX-02-009314-MONOMER; -.
- DR GO; GO:0055624; C:membrane fraction; IDA.
- DR GO; GO:0016028; C:rhabdomere; IDA.
- DR GO; GO:005515; F:protein binding; IPI.
- DR InterPro; IPR00698; Arrestin.
- DR InterPro; IPR011022; Arrestin_C.

DR	InterPro; IPR011021; Arrestin_N.	RL	Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR	PANTHER; PTHR11792; Arrestin_1.	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
DR	Pfam; PF02752; Arrestin_C; 1.	CC	Distributed under the Creative Commons Attribution-NoDerivs license
DR	PRINTS; PR00309; ARRESTIN.	CC	-----
DR	PRODOM; PD002099; Arrestin; 2.	DR	EMBL; AJ544225; CAD66650.1; - ; Genomic_DNA.
DR	PROSITE; PS00295; ARRESTINS; 1.	FT	NON_TER 18 18
KW	Complete proteome; Phosphorylation; Sensory transduction; vision.	SQ	SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
FT	CHAIN 1 364 Phosrestin-2.	FT	/FTId=PRO_0000205215.
FT	Query Match 5.2%; Score 20; DB 1; Length 364;	FT	Best Local Similarity 100.0%; Pred. No. 1e-10;
SQ	Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	228 VKKIKAMVQQGVDVLFQNG 247	QY	1 MVYNFKVFKKCAGNGKVT 18
Db	227 VKKIKAMVQQGVDVLFQNG 246	Db	1 MVYNFKVFKKCAGNGKVT 18
RESULT 7	Q7YT9 ANOST	RESULT 9	Q7YT9 ANOAR
ID	Q7YT9 ANOST	ID	Q7YT9 ANOAR
AC	Q7YT9;	AC	Q7YT9_ANOAR
DT	01-OCT-2003, integrated into UniProtKB/TREMBL.	DT	01-OCT-2003, integrated into UniProtKB/TREMBL.
DT	01-OCT-2003, sequence version 1.	DT	01-OCT-2003, sequence version 1.
DT	07-FEB-2006, entry version 6.	DT	07-FEB-2006, entry version 6.
DE	Arrestin (Fragment).	DE	Arrestin (Fragment).
GN	Name=arrl;	GN	Name=arrl;
OS	Anopheles stephensi (Indo-Pakistan malaria mosquito).	OS	Anopheles arabiensis (Mosquito).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;	OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC	Anophelinae; Anopheles; stephensi species complex.	OC	Anophelinae; Anopheles.
OX	NCBI_TaxID=30069;	OX	NCBI_TaxID=7173;
RN	NUCLEOTIDE SEQUENCE.	RN	[1]
RP	Favia G.' ricci I.' Casiraghi M.' Esposito F.';	RP	Favia G.' ricci I.' Casiraghi M.' Esposito F.';
RA	Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.	RA	Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RL		RL	
CC		CC	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License	CC	Distributed under the Creative Commons Attribution-NoDerivs License
DR	EMBL; AJ544226; CAD66651.1; - ; Genomic_DNA.	DR	EMBL; AJ544224; CAD66649.1; - ; Genomic_DNA.
DR	NON_TER 18 18	FT	NON_TER 18 18
FT	SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;	FT	SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
SQ	Query Match 4.7%; Score 18; DB 2; Length 18;	QY	1 MVYNFKVFKKCAGNGKVT 18
Query Match Best Local Similarity 100.0%; Pred. No. 7.5e-10; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1 MVYNFKVFKKCAGNGKVT 18	
QY	1 MVYNFKVFKKCAGNGKVT 18	Db	1 MVYNFKVFKKCAGNGKVT 18
Db	1 MVYNFKVFKKCAGNGKVT 18	RESULT 10	ARR1_CALVI
RESULT 8	Q7YT9_9DIPT	ID	ARR1_CALVI
Q7YT9_9DIPT	PRELIMINARY; PRT; 18 AA.	STANDARD;	PRT; 363 AA.
ID	Q7YT9_9DIPT	AC	P51486;
AC	Q7YT9_9DIPT	DT	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT	01-OCT-2003, integrated into UniProtKB/TREMBL.	DT	01-OCT-1996, sequence version 1.
DT	01-OCT-2003, sequence version 1.	DT	07-FEB-2006, entry version 28.
DT	07-FEB-2006, entry version 6.	DE	Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).
DE	Arrestin (Fragment).	GN	Name=ARR1;
GN	Name=arrl;	OS	Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
OS	Anopheles pharoensis.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;	OC	Caliphoridae; Calliphora.
NCBI_TaxID=221566;	NCBI_TaxID=221566;	NCBI_TaxID=7373;	NCBI_TaxID=7373;
RN	[1]	RN	NUCLEOTIDE SEQUENCE [mRNA].
RP	TISSUE=Retina;	RC	MEDLINE=95014564; PubMed=7929436;
RC	MEDLINE=95014564; PubMed=7929436;	RA	Plangger A., Malicki D., Whitney M., Paulsen R.;
RA	"Mechanism of arrestin 2 function in rhabdomeric photoreceptors.";	RT	

RL J. Biol. Chem. 269:26969-26975(1994); Score 16; DB 1; Length 381;
 CC -!- SIMILARITY: Belongs to the arrestin family.
 CC
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 CC
 DR EMBL; X79072; CAA55672.1; -; mRNA.
 DR PIR; A55081; A55081.
 DR HSSP; P17870; 1G4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR KW Sensory transduction; Vision.
 FT CHAIN 1 363 AA; Phosrestin-2.
 FT /FTId=PRO_0000205214.
 SQ SEQUENCE 363 AA; 40680 MW; 7C345D818E46C23E CRC64;

Query Match 4.2%; Score 16; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MVYNFKVFKKCAPNGK 16
 1 MVYNFKVFKKCAPNGK 16

RESULT 12

RBRESULT 12

DR Q6X126_DROYA PRELIMINARY; PRT; 52 AA.

ID Q6X126_DROYA ID

AC 06X126; AC

DT 05-JUL-2004, integrated into UniProtKB/TREMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE Similar to Drosophila melanogaster CG5711 (Fragment).

GN Name-Arr1.

OS Drosophila yakuba (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7245;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;

RA Domazet-Loso T.; Rautz D.; RT

RL "An evolutionary analysis of orphan genes in Drosophila." Genome Res. 13:2213-2219(2003).

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CC

DR EMBL; AY232006; AAR10029.1; -; mRNA.

DR HSSP; P08168; 1AYR.

DR FlyBase; FBgn0068531; Dyak\Arr1.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR00698; Arrestin.

DR PANTHER; PTHR11792; Arrestin_N.

DR Pfam; PF00339; Arrestin_N; 1.

DR ProDom; PD002099; Arrestin; 1.

FT NON_TER 1 1

FT NON_TER 52 52

SQ SEQUENCE 52 AA; 6166 MW; 081C148570B5EB6F CRC64;

Query Match 3.7%; Score 14; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 VEPIDGIWLDDEY 46
 33 VEPIDGIWLDDEY 46

RESULT 13

RBLRESULT 13

DR ARRH_LIMPO STANDARD; PRT; 400 AA.

ID ARRH_LIMPO ID

AC P51484; AC

DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-1996, sequence version 1.

DT 07-FEB-2006, entry version 26.

DE Arrestin, lateral eye.

OS Limulus polyphemus (Atlantic horseshoe crab).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

OC Limulidae; Limulus.

OX NCBI_TaxID=6850;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Retina;

RX MEDLINE=95096819; PubMed=7798902;

RA Smith W.C., Greenberg R.M., Calman B.G., Hendrix M.M., Hutchinson L.,

SEQUENCE 381 AA; 42747 MW; 84BB92B1BB3DA573 CRC64;

FT /FTId=PRO_000205220.

FT SQ

RA Donoso L.A., Battelle B.-A.;
 RT "Isolation and expression of an arrestin cDNA from the horseshoe crab
 RT lateral eye.";
 RL J. Neurochem. 64:1-13(1995).
 CC -!- FUNCTION: Plays an important role in the photoreceptor
 transduction.

CC -!- PTM: Phosphorylated.

CC -!- SIMILARITY: Belongs to the arrestin family.

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CC

DR EMBL; U08883; AAA82007.1; -; mRNA.
 DR HSSP; P17870; 1G4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Phosphorylation; Sensory transduction; Vision.
 FT CHAIN 1 400 Arrestin; lateral eye.
 FT SEQUENCE 400 AA; 44302 MW; F30D0D25BC2BHE33 CRC64;
 /FTId=PRO 0000205219.

Query Match 3.4%; Score 13; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FRYGGREEDEVNGL 73
 Db 68 FRYGGREEDEVNGL 80

RESULT 14

ARRH LOCMI	STANDARD;	PRT;	407 AA.
AC P32122;	DT 01-OCT-1993,	integrated into UniProtKB/Swiss-Prot.	
DT 01-OCT-1993,	sequence version 1.		
DT 07-FEB-2006,	entry version 33.		
DE Arrestin homolog.			
OS Locusta migratoria (migratory locust).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acrideromorpha; Acriidoidea; Acridae; Oedipodinae; Locusta.			
OC NCBI_TaxID=7004;			
RN [1]			
RP NUCLEOTIDE SEQUENCE.			
RC TISSUE=Endometrium;			
RG The German cDNA Consortium;			
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiapp A., Wiemann S.,			
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M.,			
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.			
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CC Distributed under the Creative Commons Attribution-NoDerivs License			
DR EMBL; CR749218; CAH18075.1; -; mRNA.			
DR SMR; Q68DZ5; 1-169.			
DR Ensembl; ENSG00000141480; Homo sapiens.			
DR GO; GO:0007600; P:sensory perception; IEA.			
DR GO; GO:0007165; P:signal transduction; IEA.			
DR InterPro; IPR000698; Arrestin.			
DR InterPro; IPR011022; Arrestin_C.			
DR PANTHER; PTHR11792; Arrestin_1.			
DR Pfam; PF02752; Arrestin_C; 1.			
DR ProDom; PD002099; Arrestin; 1.			
KW Hypothetical protein.			
SQ SEQUENCE 217 AA; 24363 MW; 61653F5BABCBBOFD CRC64;			

Query Match 2.9%; Score 11; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFFVLMHPKP 351
 Db 147 ELFFVLMHPKP 157

Search completed: May 20, 2006, 23:15:29
 Job time : 302 secs

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CC

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CC

DR EMBL; S57174; AAB25860.1; -; mRNA.

DR PIR; A56607.

DR HSSP; P17870; 1G4M.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR PANTHER; PTHR11792; Arrestin_1.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.

DR ProDom; PD002099; Arrestin; 2.

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:15:44 ; Search time 49 Seconds
 (without alignments)
 684.168 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 383
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 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
 Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649349

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	11	2.9	382	Sequence 8, Appli
2	11	2.9	409	Sequence 4, Appli
3	11	2.9	409	Sequence 7, Appli
4	9	2.3	388	Sequence 5, Appli
5	9	2.3	388	Sequence 6, Appli
6	8	2.1	279	Sequence 27414, A
7	8	2.1	315	Sequence 9940, Ap
8	8	2.1	401	Sequence 8383, AP
9	8	2.1	401	Sequence 8384, AP
10	8	2.1	410	Sequence 1, Appli
11	8	2.1	418	Sequence 2, Appli
12	8	2.1	418	Sequence 3, Appli
13	7	1.8	8	Sequence 4, Appli
14	7	1.8	8	Sequence 5, Appli
15	7	1.8	8	Sequence 6, Appli
16	7	1.8	9	Sequence 7, Appli
17	7	1.8	9	Sequence 8, Appli
18	7	1.8	9	Sequence 9, Appli
19	7	1.8	9	Sequence 10, Appli
20	7	1.8	9	Sequence 11, Conservati
21	7	1.8	9	Sequence 12, Conservati
22	7	1.8	10	Sequence 13, Conservati
23	7	1.8	10	Sequence 14, Conservati
24	7	1.8	10	Sequence 15, Conservati
25	7	1.8	11	Sequence 16, Conservati
26	7	1.8	11	Sequence 17, Conservati

ALIGNMENTS

Sequence 2490, AP
 Sequence 2513, AP
 Sequence 11937, A
 Sequence 20525, A
 Sequence 20528, A
 Sequence 20555, A
 Sequence 24797, A
 Sequence 31920, A
 Sequence 31952, A
 Sequence 28, Appli
 Sequence 28, Appli
 Sequence 28, Appli
 Sequence 8, Appli
 Sequence 46501, A
 Sequence 54, Appli
 Sequence 54, Appli
 Sequence 54, Appli
 Sequence 54, Appli
 Sequence 54, Appli

RESULT 1
 US-09-880-137-8
 ; Sequence 8, Application US/09880137
 ; Patent No. 6640025
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernstein, Gabriel
 ; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; FILE REFERENCE: MNI-131
 ; CURRENT APPLICATION NUMBER: US/09/880, 137
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: US 60/186, 706
 ; PRIORITY FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
 ; US-09-880-137-8

Query Match Best Local Similarity 2.9%; Score 11; DB 2; Length 382;
 Matches 11; Conservati 100.0%; Pred. No. 0.035; Mismatches 0; Indels 0; Gaps 0;

Qy	341	ELPFVLMHPKP	351
Db	339	ELPFVLMHPKP	349

RESULT 2
 US-09-880-137-4
 ; Sequence 4, Application US/09880137
 ; Patent No. 6640025
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernstein, Gabriel
 ; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; FILE REFERENCE: MNI-131
 ; CURRENT APPLICATION NUMBER: US/09/880, 137
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: US 60/186, 706
 ; PRIORITY FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 409

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

Query Match 2.9%; Score 11; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.037; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 3
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

Query Match 2.9%; Score 11; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.037; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 4
US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-5

Query Match 2.9%; Score 11; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.037; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 5
US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match 2.3%; Score 9; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 3.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVFVDHV 30
Db 19 GKRDVFVDHV 27

RESULT 6
US-09-252-991A-27414
; Sequence 27414, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27414
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27414

Query Match 2.1%; Score 8; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 22; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GELSAELP 343
Db 30 GELSAELP 37

RESULT 7
US-09-949-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

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CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9940
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9940

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; Matches 8; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 22 GKRDVFV рд 29
; Db 24 GKRDVFV рд 31

RESULT 8
; Sequence 8383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8383
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8383

Query Match 2.1%; Score 8; DB 2; Length 401;
; Best Local Similarity 100.0%; Pred. No. 30;
; Matches 8; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 22 GKRDVFV рд 29
; Db 6 GKRDVFV рд 13

RESULT 9
; Sequence 8384, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

Query Match 2.1%; Score 8; DB 2; Length 418;
; Best Local Similarity 100.0%; Pred. No. 31;
; Matches 8; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 22 GKRDVFV рд 29
; Db 6 GKRDVFV рд 13

RESULT 10
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-3

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; Best Local Similarity 100.0%; Pred. No. 31;
; Matches 8; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 22 GKRDVFV рд 29
; Db 23 GKRDVFV рд 30

RESULT 11
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; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-880-137-1

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; Best Local Similarity 100.0%; Pred. No. 31;
; Matches 8; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

QY 22 GKRDVFV р 29
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 23 GKRDVFV р 30

Db

RESULT 12
 US-09-880-137-2
 ; Sequence 2, Application US/09880137
 ; Patent No. 6640025
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernstein, Gabriel
 ; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
 ; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; FILE REFERENCE: MNI-131
 ; CURRENT APPLICATION NUMBER: US/09/880, 137
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIORITY NUMBER: US 60/186, 706
 ; PRIORITY FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-137-2

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 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVFV р 29
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 23 GKRDVFV р 30

Db

RESULT 13
 US-09-641-528B-2512
 ; Sequence 2512, Application US/09641528B
 ; Patent No. 702643
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Grey, Howard
 ; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 ; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 ; FILE REFERENCE: 2060.0100001
 ; CURRENT APPLICATION NUMBER: US/09/641, 528B
 ; CURRENT FILING DATE: 2000-08-15
 ; PRIORITY NUMBER: US 60/172, 705
 ; PRIORITY FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 51505
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2512
 ; LENGTH: 8
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
 ; US-09-641-528B-2512

Query Match 1.8%; Score 7; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5e+05; 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 ASTTLLA 309
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 2 ASTTLLA 8

Db

RESULT 14
 US-09-641-528B-20553
 ; Sequence 31963, Application US/09641528B
 ; Patent No. 702643
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Grey, Howard
 ; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 ; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 ; FILE REFERENCE: 2060.0100001
 ; CURRENT APPLICATION NUMBER: US/09/641, 528B
 ; CURRENT FILING DATE: 2000-08-15
 ; PRIORITY NUMBER: US 60/172, 705
 ; PRIORITY FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 51505
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 31963
 ; LENGTH: 8
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
 ; US-09-641-528B-31963

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 Best Local Similarity 100.0%; Pred. No. 5e+05; 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 ASTTLLA 309
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 2 ASTTLLA 8

Db

, " Tue May 23 13:30:39 2006

us-10-056-405-2.ol.i.rai

Page 5

Search completed: May 20, 2006, 23:17:11
Job time : 50 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:27:39 ; Search time 181 Seconds
 (without alignments)
 980.173 Million cell updates/sec

Title: US-10-056-405-2
 perfect score: 383
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 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
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Word size : 1

Total number of hits satisfying chosen parameters: 2096531

Minimum DB seq length: 0
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 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
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 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	383	100.0	383	Sequence 2, Appli
3	383	100.0	383	Sequence 238, App
4	20	5.2	364	Sequence 18, Appli
5	20	5.2	364	Sequence 12000, A
6	11	2.9	382	Sequence 8, Appli
7	11	2.9	382	Sequence 8, Appli
8	11	2.9	398	Sequence 25, Appli
9	11	2.9	398	Sequence 241, Appli
10	11	2.9	401	Sequence 27, Appli
11	11	2.9	401	Sequence 12684, A
12	11	2.9	409	Sequence 4, Appli
13	11	2.9	409	Sequence 7, Appli
14	11	2.9	409	Sequence 4, Appli
15	11	2.9	409	Sequence 7, Appli
16	11	2.9	410	Sequence 54, Appli
17	11	2.9	466	Sequence 31, Appli
18	11	2.9	479	Sequence 3, Appli
19	11	2.9	492	Sequence 4, Appli
20	9	2.3	388	Sequence 5, Appli
21	9	2.3	388	Sequence 6, Appli
22	9	2.3	388	Sequence 5, Appli
23	9	2.3	388	Sequence 6, Appli
24	9	2.3	470	Sequence 6, Appli
25	8	2.1	38	Sequence 134, Ap
26	8	2.1	48	Sequence 40768, A
27	8	2.1	63	Sequence 154582, A

ALIGNMENTS

28	8	2.1	153	4 US-10-424-999-148204	Sequence 148204, Ap
29	8	2.1	204	4 US-10-335-977-7580	Sequence 7580, Ap
30	8	2.1	208	4 US-10-767-701-41403	Sequence 41403, Ap
31	8	2.1	212	4 US-10-106-698-4673	Sequence 224408, Ap
32	8	2.1	235	4 US-10-424-599-224408	Sequence 4673, Ap
33	8	2.1	235	6 US-11-087-099-1956	Sequence 1956, Ap
34	8	2.1	270	4 US-10-767-701-38282	Sequence 38282, A
35	8	2.1	307	4 US-10-425-115-244452	Sequence 244452, Ap
36	8	2.1	366	4 US-10-335-977-7581	Sequence 7581, Ap
37	8	2.1	369	5 US-10-450-763-43933	Sequence 43933, A
38	8	2.1	410	3 US-09-880-137-3	Sequence 3, Appli
39	8	2.1	410	3 US-09-800-137A-3	Sequence 1, Appli
40	8	2.1	418	3 US-09-880-137-1	Sequence 2, Appli
41	8	2.1	418	3 US-09-880-137-2	Sequence 1, Appli
42	8	2.1	418	3 US-09-800-137A-1	Sequence 2, Appli
43	8	2.1	418	3 US-09-800-137A-2	Sequence 348, App
44	8	2.1	418	4 US-10-043-487-348	Sequence 216, App
45	8	2.1	418	5 US-10-745-237-216	

RESULT 2

US-10-056-405-2
; Sequence 2, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: N7841
; CURRENT APPLICATION NUMBER: US/10/056, 405
; CURRENT FILING DATE: 2002-01-24
; PRIORITY APPLICATION NUMBER: 60/264, 649
; PRIORITY FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
; US-10-056-405-2

Query Match 100.0%; Score 383; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 383; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVFKKCAPNGKVLYMGRDFDVHSGVVERPIDGIVVLDEYIRDNRKVFGQIVCS 60
1 MVYNFKVFKKCAPNGKVLYMGRDFDVHSGVVERPIDGIVVLDEYIRDNRKVFGQIVCS 60

Db 61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120
61 FRYGREEDEVMLNFOKECLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTNIS 120

Qy 121 PNAPSSVTLQQGEDDNGDPGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
121 PNAPSSVTLQQGEDDNGDPGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLGERIGVNICIRNNSNKMKKKIKAMVQGVD 240
181 QPCTLVRKDFMLSPGELELEVTLDKQLYLGERIGVNICIRNNSNKMKKKIKAMVQGVD 240

Qy 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKORRGIALDGQIKRDO 300
241 VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKORRGIALDGQIKRDO 300

Db 301 CLASTILLAOPDORDAFGVIIISAVVKFLGALGGELSAELPPVLMHPKPGTKAKVHA 360
301 CLASTILLAOPDORDAFGVIIISAVVKFLGALGGELSAELPPVLMHPKPGTKAKVHA 360

Qy 361 DSQADVETFRQDTIDQASVDFE 383
361 DSQADVETFRQDTIDQASVDFE 383

Db 361 DSQADVETFRQDTIDQASVDFE 383
361 DSQADVETFRQDTIDQASVDFE 383

RESULT 4

US-10-745-237-18
; Sequence 18, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P015819WO CYK
; CURRENT APPLICATION NUMBER: US 60/439, 123
; CURRENT FILING DATE: 2003-12-23
; PRIORITY APPLICATION NUMBER: US 60/468, 402
; PRIORITY FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: AAF53644
; FEATURE:
; OTHER INFORMATION: GI:7298421
; US-10-745-237-18

Query Match 5.2%; Score 20; DB 5; Length 364;

RESULT 3

US-10-954-778-238
; Sequence 238, Application US/10954778
; Publication No. US20050153368A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
; FILE REFERENCE: N1125
; CURRENT APPLICATION NUMBER: US/10/954, 778
; CURRENT FILING DATE: 2004-09-30
; PRIORITY APPLICATION NUMBER: 10/056, 405
; PRIORITY FILING DATE: 2002-01-24
; PRIORITY APPLICATION NUMBER: 60/264, 649

Best Local Similarity 100.0%; Pred. No. 3.4e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

QY 228 VKKIKAMVQQGVDFVLFQNG 247
||||||| ||||| |||||
Db 227 VKKIKAMVQQGVDFVLFQNG 246

RESULT 5
US-11-097-143-12000

; Sequence 12000, Application US/11097143
; Publication No. US20050208558A1

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR FILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: 60/191,637

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-880-137-8

Query Match 2.9%; Score 11; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMLHPKP 351
|||||||
Db 339 ELPFVLMLHPKP 349

RESULT 7
US-09-800-137A-8

; Sequence 8, Application US/09800137A
; Publication No. US20030157553A1

GENERAL INFORMATION:

APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12000

LENGTH: 364

TYPE: PRT

ORGANISM: DROSOPHILA

US-11-097-143-12000

Query Match 5.2%; Score 20; DB 6; Length 364;

Best Local Similarity 100.0%; Pred. No. 3.4e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

QY 228 VKKIKAMVQQGVDFVLFQNG 247
||||||| |||||
Db 227 VKKIKAMVQQGVDFVLFQNG 246

RESULT 6
US-09-880-137-8

; Sequence 8, Application US/09880137
; Patent No. US20020031295A1

GENERAL INFORMATION:

APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094, 240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 25

LENGTH: 398

TYPE: PRT

ORGANISM: Anopheles gambiae

US-10-094-240-25

Query Match 2.9%; Score 11; DB 4; Length 398;

Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0;

Matches 11; Conservative 0; Mismatches 0;

QY 62 RYGRREDEVNG 72
|||||||

Db 61 RYGREEDEVMG 71
 RESULT 9
 US-10-954-778-241
 ; Sequence 241, Application US/10954778
 ; Publication No. US20050153368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZWIEBEL, LAURENCE J.
 ; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
 ; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
 ; FILE REFERENCE: N1125
 ; CURRENT APPLICATION NUMBER: US/10/954, 778
 ; CURRENT FILING DATE: 2004-09-30
 ; PRIOR APPLICATION NUMBER: 10/056, 405
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/264, 649
 ; PRIOR FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 241
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Anopheles gambiae
 ; US-10-954-778-241

Query Match 2.9%; Score 11; DB 5; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 62 RYGREEDEVMG 72
 Db 61 RYGREEDEVMG 71

RESULT 10
 US-10-094-240-27
 ; Sequence 27, Application US/10094240
 ; Publication No. US20030082637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZWIEBEL, LAURENCE J.
 ; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
 ; FILE REFERENCE: N8289
 ; CURRENT APPLICATION NUMBER: US/10/094, 240
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 10/056, 405
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/264, 649
 ; PRIOR FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-10-094-240-27

Query Match 2.9%; Score 11; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 62 RYGREEDEVMG 72
 Db 61 RYGREEDEVMG 71

RESULT 11
 US-11-097-143-12684
 ; Sequence 12684, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; et al.

RESULT 12
 US-09-880-137-4
 ; Sequence 4, Application US/09880137
 ; Patent No. US20020031295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernstein, Gabriel
 ; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 ; FILE REFERENCE: MNTI-131
 ; CURRENT APPLICATION NUMBER: US/09/880, 137
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: US 60/186, 706
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-137-4

Query Match 2.9%; Score 11; DB 3; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 13
 US-09-880-137-7
 ; Sequence 7, Application US/09880137
 ; Patent No. US20020031295A1

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; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-880-137-7

Query Match 2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 14
US-09-800-137A-4
; Sequence 4, Application US/09800137A
; Publication No. US20030157553A1

; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-800-137A-4

Query Match 2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 15
US-09-800-137A-7
; Sequence 7, Application US/09800137A
; Publication No. US20030157553A1

; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-800-137A-7

Query Match 2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

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Job time : 182 secB

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:27:49 ; Search time 10 Seconds
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Title: US-10-056-405-2
 Perfect score: 383
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 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
 Searched: 21570 seqs, 2136119 residues

Word size : 1

Total number of hits satisfying chosen parameters: 21565

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	11	2.9	409	Sequence 173, App
2	7	1.8	709	Sequence 31, App
3	7	1.8	710	Sequence 33, App
4	7	1.8	711	Sequence 12, App
5	7	1.8	711	Sequence 15, App
6	7	1.8	711	Sequence 17, App
7	7	1.8	711	Sequence 18, App
8	7	1.8	711	Sequence 21, App
9	7	1.8	711	Sequence 27, App
10	7	1.8	711	Sequence 30, App
11	7	1.8	711	Sequence 15, App
12	7	1.8	993	Sequence 18, App
13	6	1.6	34	Sequence 21, App
14	6	1.6	130	Sequence 24, App
15	6	1.6	142	Sequence 30, App
16	6	1.6	178	Sequence 34, App
17	6	1.6	283	Sequence 2437, App
18	6	1.6	353	Sequence 2463, App
19	6	1.6	363	Sequence 2464, App
20	6	1.6	363	Sequence 2465, App
21	6	1.6	411	Sequence 2466, App
22	6	1.6	419	Sequence 2467, App
23	6	1.6	440	Sequence 2468, App
24	6	1.6	456	Sequence 2469, App
25	6	1.6	457	Sequence 2470, App

ALIGNMENTS

RESULT 1
 US-10-505-928-173
 ; Sequence 173, Application US/10505928
 ; Publication No. US200601088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505, 928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIORITY APPLICATION NUMBER: US 60/363, 019
 ; PRIORITY FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 173
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-505-928-173

Query Match Best Local Similarity 2.9%; Score 11; DB 6; Length 409;
 Matches 11; Conservativeness 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Q	341	ELPFVILMHPKP	351
Db	339	ELPFVILMHPKP	349

RESULT 2
 US-11-258-767-31
 ; Sequence 31, Application US/11258767
 ; Publication No. US20060094082A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Varadacharya, Atul
 ; APPLICANT: Glynn, Peter
 ; APPLICANT: Petrank, Karel
 ; APPLICANT: Engelmayr, Jose
 ; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 ; FILE REFERENCE: HO-P02915US1
 ; CURRENT APPLICATION NUMBER: US/11/258, 767
 ; CURRENT FILING DATE: 2005-10-26
 ; PRIORITY APPLICATION NUMBER: US 60/622, 176
 ; PRIORITY FILING DATE: 2004-10-26
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 31
 ; LENGTH: 709

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; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-31

Query Match 1.8%; Score 7; DB 7; Length 709;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 7 LFLGALG 13

RESULT 3
US-11-258-767-33
; Sequence 33, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadacharya, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Pettrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 710
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-33

Query Match 1.8%; Score 7; DB 7; Length 710;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 LFLGALG 15

RESULT 4
US-11-258-767-12
; Sequence 12, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadacharya, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Pettrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-12

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 LFLGALG 15

RESULT 5
US-11-258-767-15
; Sequence 15, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadacharya, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Pettrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-15

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 LFLGALG 15

RESULT 6
US-11-258-767-17
; Sequence 17, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadacharya, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Pettrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-17

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 LFLGALG 15

RESULT 7
US-11-258-767-18
; Sequence 18, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:

```

APPLICANT: Varadhachary, Atul
 APPLICANT: Glynn, Peter
 APPLICANT: Pettrak, Karel
 APPLICANT: Engelmayr, Jose
 TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 FILE REFERENCE: HO-P02915US1
 CURRENT APPLICATION NUMBER: US/11/258,767
 CURRENT FILING DATE: 2005-10-26
 PRIOR APPLICATION NUMBER: US 60/622,176
 PRIOR FILING DATE: 2004-10-26
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 18
 LENGTH: 711
 TYPE: PRT
 ORGANISM: HUMAN
 US-11-258-767-18

Query Match 1.8%; Score 7; DB 7; Length 711;
 Best Local Similarity 100.0%; Pred. No. 8.3; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Publication No. US20060094082A1

GENERAL INFORMATION:
 APPLICANT: Varadhachary, Atul
 APPLICANT: Glynn, Peter
 APPLICANT: Pettrak, Karel
 APPLICANT: Engelmayr, Jose
 TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 FILE REFERENCE: HO-P02915US1
 CURRENT APPLICATION NUMBER: US/11/258,767
 CURRENT FILING DATE: 2005-10-26
 PRIOR APPLICATION NUMBER: US 60/622,176
 PRIOR FILING DATE: 2004-10-26
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 21
 LENGTH: 711
 TYPE: PRT
 ORGANISM: HUMAN
 US-11-258-767-21

RESULT 8
 US-11-258-767-21
 ; Sequence 21, Application US/11258767
 ; Publication No. US20060094082A1

GENERAL INFORMATION:
 APPLICANT: Varadhachary, Atul
 APPLICANT: Glynn, Peter
 APPLICANT: Pettrak, Karel
 APPLICANT: Engelmayr, Jose
 TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 FILE REFERENCE: HO-P02915US1
 CURRENT APPLICATION NUMBER: US/11/258,767
 CURRENT FILING DATE: 2005-10-26
 PRIOR APPLICATION NUMBER: US 60/622,176
 PRIOR FILING DATE: 2004-10-26
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 30
 LENGTH: 711
 TYPE: PRT
 ORGANISM: HUMAN
 US-11-258-767-30

RESULT 10
 US-11-258-767-30
 ; Sequence 30, Application US/11258767
 ; Publication No. US20060094082A1

GENERAL INFORMATION:
 APPLICANT: Varadhachary, Atul
 APPLICANT: Glynn, Peter
 APPLICANT: Pettrak, Karel
 APPLICANT: Engelmayr, Jose
 TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 FILE REFERENCE: HO-P02915US1
 CURRENT APPLICATION NUMBER: US/11/258,767
 CURRENT FILING DATE: 2005-10-26
 PRIOR APPLICATION NUMBER: US 60/622,176
 PRIOR FILING DATE: 2004-10-26
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 30
 LENGTH: 711
 TYPE: PRT
 ORGANISM: HUMAN
 US-11-258-767-30

RESULT 9
 US-11-258-767-27
 ; Sequence 27, Application US/11258767
 ; Publication No. US20060094082A1

GENERAL INFORMATION:
 APPLICANT: Varadhachary, Atul
 APPLICANT: Glynn, Peter
 APPLICANT: Pettrak, Karel
 APPLICANT: Engelmayr, Jose
 TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 FILE REFERENCE: HO-P02915US1
 CURRENT APPLICATION NUMBER: US/11/258,767
 CURRENT FILING DATE: 2005-10-26
 PRIOR APPLICATION NUMBER: US 60/622,176
 PRIOR FILING DATE: 2004-10-26
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 34
 LENGTH: 711
 TYPE: PRT
 ORGANISM: HUMAN
 US-11-258-767-34

Query Match 1.8%; Score 7; DB 7; Length 711;
 Best Local Similarity 100.0%; Pred. No. 8.3; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 329 LFLGALG 335
 Db 9 LFLGALG 15

RESULT 12

US-10-511-937-2463

; Sequence 2463, Application US/10511937

; Publication No. US20060088836A1

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: FRY, Kirk

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
 TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 2463

; LENGTH: 993

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-511-937-2463

Query Match 1.8%; Score 7; DB 6; Length 993;
 Best Local Similarity 100.0%; Pred. No. 12; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 50 NRKVFGQ 56
 Db 488 NRKVFGQ 494

RESULT 13

US-10-706-435A-24

; Sequence 24, Application US/10706435A

; Publication No. US20060088547A1

; GENERAL INFORMATION:

; APPLICANT: Walter Reed Army Institute of Research

; APPLICANT: Lanar, David E.

; APPLICANT: Hillier, Collette J.

; APPLICANT: Lyon, Jeffrey A.

; APPLICANT: Angov, Evelina

; APPLICANT: Kumar, Sanjai

; APPLICANT: Rogers, William

; APPLICANT: Barbosa, Arnoldo

; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
 FILE REFERENCE: 003/285/SAP

; CURRENT APPLICATION NUMBER: US/10/706,435A

; PRIOR FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: 60/425,719

PRIOR FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 156

SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Consensus amino acid sequence

; US-10-370-959-30

Query Match 1.6%; Score 6; DB 6; Length 130;
 Best Local Similarity 100.0%; Pred. No. 19; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

Qy 104 LLKKLG 109
| | | |
Db 3 LLKKLG 8

RESULT 15
US-10-511-937-2437

; Sequence 2437, Application US/10511937

Publication No. US20060088836A1

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Wohlgemuth, Jay

APPLICANT: FRY, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

APPLICANT: Prentice, James

APPLICANT: Morris, MacDonald

APPLICANT: Rosenberg, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOsing

TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2437

LENGTH: 142

TYPE: PRT

ORGANISM: HOMO sapiens

US-10-511-937-2437

Query Match 1.6%; Score 6; DB 6; Length 142;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 KKLGSN 111
| | | |

Db 16 KKLGSN 21

Search completed: May 20, 2006, 23:31:05

Job time : 10 secs

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